GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                           00000000
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                                     length: 0
length: 2000000000
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33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna,
2: /cgn2_6/ptodata/2/pubpna,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       538826 seqs, 387737923 residues
                                                                                                                                                                                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                 Query
                     53.9
53.9
53.9
53.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                             249487
2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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                                   3266
1176
1479
6395
6425
6439
6446
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7685
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10 US-09-983-797-3

9 US-09-962-527-1

9 US-09-962-527-2

9 US-09-962-527-2

9 US-09-962-527-4

9 US-09-962-527-4

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9 US-09-949-317-22

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0 US-09-925-301-233

US-10-098-841-213

US-09-954-531-130
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2938.192 Million cell updates/sec
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Sequence 457, App
Sequence 3, Appli
Sequence 213, App
Sequence 213, App
Sequence 310, App
Sequence 310, App
Sequence 938, App
Sequence 938, App
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 25, Appli
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45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	ω 11	30	29	28	27	26	25	24	23	22	21	20	
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10	10	9	9	9	10	10	10	9	10	9	9	10	10	10	10	10	9	φ	9	9	9	9	9	9	9	
US-09-795-668-752	US-09-795-668-751	US-09-946-807-753	US-09-946-807-752	US-09-946-807-751	US-09-878-574-7659	US-09-764-847-1020	US-09-764-847-1019	US-10-184-832-4	US-09-764-847-31	US-09-954-531-1363	US-09-938-842A-21	US-09-770-444-240	US-09-923-876-1950	US-09-867-701-3800	US-09-867-701-6095	US-09-978-199-3	US-09-949-316-27	-09-949-317-	316-	US-09-949-317-24	-316-	US-09-949-316-23	US-09-949-317-26	US-09-949-317-23	US-09-949-316-25	
Sequence 752, App	Sequence 751, App	•	`	Sequence 751, App	Sequence 7659, Ap	•	Sequence 1019, Ap	Sequence 4, Appli	 Sequence 31, Appl 	Sequence 1363, Ap	Ą	Sequence 240, App	'n	Sequence 3800, Ap	Sequence 6095, Ap	Sequence 3, Appli	Sequence 27, Appl	Sequence 27, Appl	-	Sequence 24, Appl	26,	Sequence 23, Appl	`	Sequence 23, Appl	Sequence 25, Appl	

ALIGNMENTS

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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 457
LENGTH: 3249
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-925-301-457; Sequence 457, Application US/09925301; Patent No. US20020052308A1
                                                                                    RESULT 2
US-10-026-188-3
                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: n equals a, t, g, or US-09-925-301-457
                                Sequence 3, Application US/10026188 Patent No. US20020164645A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA106
 APPLICANT: Zuker, Charles APPLICANT: Zhang, Yifeng
                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (3234)
                                                                                                                                                         3001 GGCAGCTCCATGCTGGAACAGAGTAGGGAATTC 3033
                                                                                                                                                                                           1 GGGGGATCCATGCCGGAACAGAGTAACGATTAC
                                                                                                                                                                                                                             l Similarity
25; Conserv
Zhang, Yifeng
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                            61.2%;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 233
LENGTH: 2081
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-301-233
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US-10-098-841-213/c
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US-09-925-301-233/c
; Sequence 233, Application US/09925301
; Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 198467 GTGGATCCATGCCAGGGAAATGAT 198495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim
Matches 23;
                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                             Sequence 213, Application US/10098841 Publication No. US20020197679A1
                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENCTH: 249487
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
                                                                                                                                     APPLICANT: Tang, APPLICANT: Liu,
                                                                    APPLICANT:
                                                                                      APPLICANT:
                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Regents of the University of California TITLE OF INVENTION: Assays for Taste Receptor Cell Specific TITLE OF INVENTION: Ion Channel ELLE REFERENCE: 02307E-114910US CURRENT APPLICATION NUMBER: US/10/026;188 CURRENT FILING DATE: 2001-12-21 PRIOR APPLICATION NUMBER: US 60/259,379 PRIOR FILING DATE: 2000-12-29 PRIOR FILING DATE: 2000-12-29 PRIOR SEQ ID NOS: 8
APPLICANT:
                                                    APPLICANT:
                                  APPLICANT:
                  PPLICANT:
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                                                                                                                                                                                                                                                                                                   396 GGGGCATCCAGGTGGGAACATCGTAAGGACTA 365
                                                                                                                                                                                                                                                                                                                                                                    Match 58.2%;
Local Similarity 75.0%;
es 24; Conservative
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                              Wang, Jian-Rui
Zhao, Qing A.
Chen, Rui-hong
                                                                    Ma, Yunging
                                                                                   Zhou, Ping
                                                                                                                   Asundi, Vinod
                Ren, Feiyan
                                                                                                                                       Liu, Chenghua
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                                                                                                   Chongjun
                                                                                                                                                             Y. Tom
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79.3%;
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Pred. No. 1
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Pred. No. 31;
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US-10-098-841-213
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PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEC
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SEQ ID NO 213
LENGTH: 5201
                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                 SEQ ID NO 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 689290-77

CURRENT APPLICATION NUMBER: US/09/954,531

CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: US/60/233,133

PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Gene Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Weaver, Zoe
                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
    3434
                                                                                                                                                                                                                              LENGTH: 5404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4476 GGAGATCCACGCAGTAACTGAGTAACTCTGAC 4445
                                                                                                Local
                                       2 GGGGATCCATGCCGGAACAGAGTAACGATTAC 33
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GGAGATCCACGCAGTAACTGAGTAACTCTGAC 3403
                                                                               l Similarity
24; Conserv
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Qian, Xiaohong B.
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Wang, Zhiwei
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                                                                                 Conservative
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                                                                                                  58.2%;
75.0%;
                                                                             9: Score 19.2; E
Pred. No. 21;
0; Mismatches
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Pred. No. 21;
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                                                                                                                     Length 5404;
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                                                                               Indels
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                                                                               0;
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RESULT 8
US-09-777-564-938/c
; Sequence 938, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Homo sapiens US-10-015-219-938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-954-531-351
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US-10-015-219-938/c
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                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493C1
CURRENT APPLICATION NUMBER: US/10/015,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 938, Application US/10015219 Publication No. US20030008299A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. US20020165180A1 GENERAL INFORMATION:
                                                                                                                                                                                                          Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 351,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1739
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/60/233,133 PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/60/234,567 PRIOR FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                                                                        ENGTH: 439
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                                                                                                                                                                                                                           Local
                                                                                                                                  97
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Local Similarity 75.0%;
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                                                                                                                                                             3 GGGATCCATGCCGGAACAGAGTAACGA 29
                                                                                                                                  GGGATCCATTCTGGAACAGAATGAAGA 71
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                                                                                                                                                                                                          Conservative
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1739
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81.5%;
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Pred. No.
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Pred. No. 21;
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18;
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US-09-917-800A-1645/c

Sequence 1645, Application US/09917800A Patent No. US20020119462A1

GENERAL

INFORMATION

APPLICANT: Mendrick, Donna APPLICANT: Porter, Mark APPLICANT: Johnson, Kory

Porter, Mark Johnson, Kory Castle, Arthur

APPLICANT:

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NAME/KEY: CDS
LOCATION: (40)..(642)
NAME/KEY: unsure
LOCATION: (1)..(3266)
OTHER IMFORMATION: n= a,
US-09-989-545-9
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RESULT 10
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                                                                                                                  Matches
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 5800-10B
CURRENT APPLICATION NUMBER: US/09/989,545
CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Manning, Stephen
APPLICANT: Coyle, Anthony J.
APPLICANT: Gutterrez-Ramos, Jose-Carlos
TITLE OF INVENTION: No. US20020164697Alel Th2-Specific Molecules and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
                                                                                                                                                                                                                                                                                               LENGTH: 3266
TYPE: DNA
ORGANISM: Mus
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/168,229
PRIOR FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lehar, Sophie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.493
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver
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TYPE: DNA
                                                                                                                                                                                                                                                                                    FEATURE:
                                               2366 GGGGATCCTTCAAGGAACAGAGTAAAG 2340
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                                                                                                                                Local
                                                                                2 GGGGATCCATGCCGGAACAGAGTAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGATCCATGCCGGAACAGAGTAACGA 29
                                                                                                               Similarity 81.9
22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Window Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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81.5%;
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81.5%;
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                                                                                                                                Score 19;
Pred. No.
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Pred. No. 18;
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Elashoff, Michael

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                                                                                                                                                          ; SEQ ID NO 3;
LENGTH: 1479;
TYPE: DNA;
ORGANISM: Arabidopsis thaliana
US-09-883-797-3
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US-09-883-797-3
; Sequence 3, Application US
; Patent No. US20020066123A1
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                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local :
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SEQ ID NO 1645
LENGTH: 1176
                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 20;
                                                                                                                                                                                                                                                                                                                              APPLICANT: Jaworski, Jan G.
APPLICANT: Post Beittenmiller, Martha A.
APPLICANT: Todd, James
TITLE OF INVENTION: FATTY ACID ELONGASES
FILE REFERENCE: 07148/064001
CURRENT APPLICATION NUMBER: US/09/883,797
CURRENT FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/868,373 PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/222,040 PRIOR FILING DATE: 2000-07-31 PRIOR APPLICATION NUMBER: US 60/222,880 PRIOR FILING DATE: 2000-11-02 PRIOR APPLICATION NUMBER: US 60/290,029 PRIOR APPLICATION NUMBER: US 60/290,029 PRIOR FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/917,800A CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/292,336 PRIOR FILING DATE: 2001-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 44921-5038-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FITLE OF INVENTION: Molecular Toxicology Modeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
  891
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                                                                                               Local Similarity
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                                    2 GGGGATCCATGCCGGAACAGAGTAACGAT 30
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GCGGGTCCATACCGGAGCAGATGACCGAT 919
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                                                                             Conservative
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                                                                                             53.9%;
75.9%;
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87.0%;
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                                                                           0,
                                                                                             Score 17.8;
Pred. No. 77;
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Pred. No. 49;
                                                                           Mismatches
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                                                                                                               Length 1479;
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                                                                           Indels
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: SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-962-527-1
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US-09-962-527-3
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US-09-962-527-1
                                                                                                                                Sequence 3, Application US/09962527
Publication No. US20030049813A1
GENERAL INFORMATION:
APPLICANT: GARGER, STEPHEN
APPLICANT: GARGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09962527
Publication No. US20030049813A1
GENERAL INFORMATION:
APPLICANT: GARGER, STEPHEN
                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.9%;
Best Local Similarity 58.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6395 base pairs
                                                                                                                                                                                                                                                                                                 3398 GGUCGAUGCAGGAACACAAUAGCAAUUAC 3426
                                                                                                                                                                                                                                                                                                                                      5 GATCCATGCCGGAACAGAGTAACGATTAC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ for Windows Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,527
FILING DATE: 24-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A PROCESS FOR ISOLATING AND PEPTIDES PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
NUMBER OF SEQUENCES:
                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/037,751 FILING DATE: 10-march-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                             HOLTZ, R. BARRY MCCULLOCH, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOLTZ, R. BARRY
MCCULLOCH, MICHAEL
TURPEN, THOMAS
                                                                             TURPEN, THOMAS
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FROM PLANT SOURCES
                                      A PROCESS FOR ISOLATING AND PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                             Score 17.8;
Pred. No. 97
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                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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0;

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TOPOLOGY: unknown;

MOLECULE TYPE: Genomic RNA
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-962-527-3
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US-09-962-527-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09962527 Publication No. US20030049813A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3398 GGUCGAUGCAGGAACACAAUAGCAAUUAC 3426
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les 17; Conserv
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                ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR WINDOWS Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,527
FILING DATE: 24-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert p
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A PROCESS FOR ISOLATING AN PURIFYING VIRUSES SOLUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 6425 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GARGER, STEPHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                    CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/037,751 FILING DATE: 10-march-1998
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APPLICATION NUMBER: US/09/962,527
                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                              HOLTZ, R. BARRY
MCCULLOCH, MICHAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1299 Pennsylvania Avenue N.W.
                                                                                                                                                      USA
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58.6%;
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Pred. No. 97;
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MOLECULE TYPE: Genomic RNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-962-527-2
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US-09-962-527-5
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3398 GGUCGAUGCAGGAACACAAUAGCAAUUAC 3426
                              APPLICATION NUMBER: 09/037,751
FILING DATE: 10-march 1998
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 00801.0
TELEPHONE: 650-463-8109
TELEPHONE: 650-463-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GATCCATGCCGGAACAGAGTAACGATTAC 33
                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,527
FILING DATE: 24-Sep-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,751
FILING DATE: 10-march-1998
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 00801.0140.999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEPAX: 650-463-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GARGER, STEPHEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: DC
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                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF INVENTION: A PROCESS FOR ISOLATING AND PURIFYING VIRUSES SOLUBLE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 6439 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                        20004
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MCCULLOCH, MICHAEL
TURPEN, THOMAS
                  <Unknown>
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58.6%;
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                                                                                                                                                                                                                                                                                                        for Windows Version
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Pred. No. 97;
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                                                                                            00801.0140.999
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SEQUENCE CHARACTERISTICS:
LENGTH: 6446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Genomic RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-962-527-5
                                                                                            В
Search completed: March 23, 2003, 17:16:40 ob time: 81.7097 secs
                                                                                                                                                                           Query Match 53.9%; Score 17.8; DB 9; Length 6446; Best Local Similarity 58.6%; Pred. No. 97; Matches 17; Conservative 5; Mismatches 7; Indels 0;
                                                                                     5 GATCCATGCCGGAACAGAGTAACGATTAC 33
| :| |:|| |||||| | :| | |::||
3398 GGUCGAUGCAGGAACACAAUAGCAAUUAC 3426
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Title:
Perfect score:
Sequence:
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                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BG
Score
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length: 2000000000
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Match
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33
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gb_est2:*
gb_htc:*
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536	524	515	493	470	467	462	450	426	417	415	410	408	396	372	364	359	355	336	320	312	309	174	613	597	571	441	1013	893	108	786	709	702	645	632	628	626	573	558
9		14																						13	17	13	14	14	12	13	12	10	13	13	13	10	13	13
AL561640		вм837087		R15962	O1	21	AA232077	T62496	Οì	\sim	O	9	23	v	F06857	F06503	w	AA309505	v	AW249313	F06359			I5948	Z1435	M2836	BQ881423	9223	7029	5224	69961	W30572	4769	Ç,	7242	Ξ	8659	483
AL561640 AL561640	K-EST012		DKF	R15962 ya47f08.rl	AV715589 AV715589	BF193212 244717 MA	zr23	rc03g	AA312757 EST183405	AV7	tg89	601	AV684237 AV684237	AA172156 zp24f11.r	SC1MH111	F06503 HSC1AD101 n	60131061	AA309505 EST180604	SC2FG101	AW249313 2819320.5	SC15F101						BQ881423 AGENCOURT			52244	614	05720	1547693 60319184	75251 fq30a09.	72422 imageqc_	34357 fi18d11	86599 fv75a03.	832 fu36f03.

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AA723009 454 bp mF Zh30005.s1 Soares_pineal_gland_N3HPG IMAGE:413600 3', mRNA sequence. AA723009 GI:2740716

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

Homo sapiens AA723009.1 EST. human.

RESULT 1
AA723009
LOCUS
DEFINITION

mRNA

Homo sapiens cDNA clone linear

EST 02-JAN-1998

ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800 1 (bases 1 to 454)
Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Hiller, L., Rilen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Walle, T., Waterston, R. and Wilson, R. Washbu-NCI human EST Project
Unpublished (1997) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence ston. 452

22.6 21.8 21.8

75.8 75.8 75.8 68.5 66.1

454 470 664 466 410 467

AA723009 AI497811

12 13 12

BG699685 BE019848 BI350717 BG892366

AA723009 zh30e05.s AI497811 tm89f05.x BG699685 602681538 BED19848 bb60e12.y BI350717 fr37c06.y BG892366 fp75d04.y

Length

DB

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Description

COMMENT

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TITLE
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Seq primer: -40UP from Gibco
High quality sequence stop: 455.
                                                                                                                                                                                                                          DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 721 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 470)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI497811 470 bp mRNA linear EST 14-APR-1999 tm89f05.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165313 3' similar to WP:C54A12.4 CE01868 RAS-RELATED PROTEIN ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /BTGAP),
                                                                                                                                                                                                                                                                                                                                                                                          cgapbs-r@mail.nih.gov
Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø
/note-"Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. Fatima Bonaldo.
                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:2165313"
/clone_lib="NCI_CGAP_Brn25"
                                                     /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                              Location/Qualifiers
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/clone="IMAGE:413600"
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84.8%;
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129

1 GGGGGATCCATGCCGGAACAGAGTAACGATTAC 33

Matches

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10709 row: k column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BG699685.1 GI:13968244
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                     Similarity
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                                                                                                     /note-*Organ: brain; Vector: pBluescriptk (modified pBluescript KS+); Site_I: BamHI; Site_Z: SalI-XhOI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.*

Institutes of Health). Note: this is a NIH_MGC Library.*
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155 c 155 g 68 t 1 others
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/clone="IMAGE:4814337"
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                   75.8%;
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84.8%;
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Pred. No.
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                                                                                                                                                                                                                                                  BI350717
410 bp mRNA linear EST 26-JUL-2002 fr37c06.yl zebrafish adult brain Danio rerio cDNA clone 4955530 5' similar to TR:095057 095057 BC41195_1.; mRNA sequence.
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                       Clark, M., Johnson, S.L.,
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                      BI350717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 466)
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                                                                   Actinopterygii, Neop
; Cyprinidae; Danio.
                                                                                                                                           Danio rerio
                                                                                                                                                                                                           BI350717.1
                                                                                                                                                              zebrafish
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                                             (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
k,M., Johnson,S.L., Lehrach,H.,
Hillier,L., Kucaba,T., Martin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3029902"
/clone="IMAGE:3029902"
/clone_lib="NHH_MGC_9"
/flssue_type="adenocarcinoma cell line"
/tlssue_type="adenocarcinoma cell line"
/tlssue_type="adenocarcinoma cell line"
/tlssue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Organ: ovary: Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5/
cloned into ECORI/XhoI sites using the following 5/
adaptor: GGCAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                               1 to 410)
                                                                                                                                                                                                              GI:15045163
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                                                                                        Neopterygii;
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Pred. No. 25;
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Martin, J.,
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                     Lee, R.,
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e,R., Li,F., Marra,M., Eddy
Beck,C., Wylie,T., Underwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                        Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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JOURNAL
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Best Local
                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATGCCGGAACAGAGTAACGATTAC 33
                                                                                                                            Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., S., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Unik, Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B. Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritte. Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters, S., Shin, M., Waters, S., Shin, M., Shin, M.,
Unpublished (1998)
Contact: Stephen L
                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; '
; Cyprinidae; Danio.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danio rerio
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4787766 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stephen L. Johnson Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1998)
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                                                                   WashU Zebrafish EST Project 1998
                                                                                                          and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG892366.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU Zebrafish EST
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. coli DH10B"
/note="Vector: p2IPLOX; Site_1: Not1; Site_2: Sal
Original library was constructed in lambdaZIPLOX excision of the cDNA library was performed to yie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pZIPLOX plasmids. Insert check was library."
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/tissue_type="brain"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="4955530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="zebrafish adult brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zebrafish adult retina cDNA Danio rerio cDNA clone similar to TR:095057 095057 BC41195_1. ; mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:14286976
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92.0%;
   Johnson
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Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             ; Craniata;
Teleostei;
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Ostariophysi;
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i; Cypriniformes
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Washington University School of Medicine

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RESULT 7
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 CATGCCGGAACAGAGTAACGATTAC 33
                                   cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenientrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                    Other_ESTs: fu36f03.x1
Other_ESTs: fu36f03.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                              Tel: 314 286 1800 Fax: 314 286 1810
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                         www.rzpd.de)
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primer:
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/note="Yector: Lambda ZAP II (pBluescript SK-);
EcoRI; Site_2: Sali; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) R2PD library number:
a 124 c 118 g 99 t 1 others
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/db_xref="taxon:7955"
/clone="4787766"
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                                                                                                                                                                                                                                                                                                                                                                                       Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: John Ngai cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Unc, K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, Swaller, G., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, Swaller, G., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, G., Gibbons,M., G., Gibb
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                                                                                                                                                                                                                                                                                                                                                      www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: zbrafish@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
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/clone_lib="zebrafish adult brain"
/sex="mixed male and female"
                                                                                                                     /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                /clone="5414284"
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/tissue_type="brain"
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S., Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B., Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R. WashU Zebrafish EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library constructed by Dr. Sumio Sugano and Sequencing by: Washington University Genome Seq primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: S.L. Johnson
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Other_ESTs: fi18d11.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1
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314 286 1810
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                                                                                        with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DrallI adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DralII sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA caccatgage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI; Original library was constructed in lambdaZIPLOX. Nexcision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

157 c 144 g 121 t
                                                                                                                                                                                           /lab host="DH10B (phage resistant)"
/lab host="DH10B (phage resistant)"
/note="Vector: pmE18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCCTTTTTTTTTTTTTTTTT];
                                                                                                                                                                                                                                                                                                   unfertilized eggs)"
/dev_stage="adult"
insert. Size selection was performed to exclude fragments (1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     /sex="mixed (one male and one female,
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Sugano Kawakami zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:7955"
/clone="2601525"
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Sequencing Center
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CATGCCGGAACAGAGTAACGATTAC
                                                      . Similarity 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: LLAM10715 ro
Seq primar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: help@image.llnl.gov
This read has been produced as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having quality control efforts with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Prange CK
The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prange, C.K.
The I.M.A.G.E. Consortium quality control effort: resequencing for verification
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kale, P.I., Harsch, T.J., Folta, P.A., Nelson, D.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              information on obtaining this clone, please contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Livermore, CA, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawrence Livermore National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammalia; Eutheria; Primates; (bases 1 to 628)
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                                                                                                                                                                                                            /note="Organ: brain; Vector: pBluescriptR (modified pBluescript RS+); Site_1: BamHI; Site_2: SalI-TADAI (dtcgag pBluescript RS+); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the
                                                                                                                                              Institutes of Health). Note: this is a NIH_MGC 175 c 197 g 116 t 1 others
                                                                                                                                                                            Cap-trapper method (Carninci, in preparation). Li
                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:4816673"
                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 59;
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                                                      Mismatches
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                                                                         59;
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Euteleostomi;

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RESULT 12
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Other_ESTs: fq30a09.x3
Contact: Stephen L. Johnson
Contact on University School of Medicine
Washington University Box 8501, St. I
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
BI547693 645 bp r 603191841F1 NIH_MGC_95 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and
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fq30a09.y3 zebrafish
similar to TR:095057
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. coli DH10B"
/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
/original library was constructed in lambdaZIPLOX. A
excision of the cDNA library was performed to yield
pZIPLOX plasmids. Insert check was done in original
library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="4832920"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="mixed male and female"
/tissue_type="brain"
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adult brain Danio rerio cDNA clone 4832920 5'
095057 BC41195_1. ;, mRNA sequence.
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Pred. No. 5
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 702)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
                                                                                                                                                                                                                           Danio rerio
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Clone distribution: MGC clone distribution information can be
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  Wilson, R.
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166 c 205 g 113 t
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/tissue_type="hippocampus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:526295"
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           Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10703 row: h column: 11
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1 (bases 1 to 709)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                       Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein
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Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Stephen L. Johnson
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/note="Vector: pZIPLOX; Site_1: Not1; Site_2: Sal1;
/note="Vector: pZIPLOX; Site_1: Not1; Site_2: Sal1;
Original library was constructed in lambdaZIPLOX. I
excision of the cDNA library was performed to yield
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189 c 181 g 137 t 1 others
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/db_xref="taxon:7955"
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/dev_stage="adult"
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High quality sequence stop: 589.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                        /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalT-Thoi (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched formalized to ROT 5. This is a primary library enriched
                      for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Li constructed by M. Brownstein (NIMH/NHGRI, National
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/db_xref="taxon:9606"
/clone="IMAGE:5275297"
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p mRNA 1 complete cds.

linear

PRI 25-JUN-2002

Homo sapiens mRNA for Di-Ras1, AB076888 AB076888.1 GI:21624247

SOURCE ORGANISM

brain cDNA. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens adult brain cDNA to mRNA, clone_lib:lambda "APII human

Kontani, K., Tada, M., Ogawa, T., Okai, T. and Katada, T. Di-Ras: A Distinct Subgroup of Ras-family GTPases with Unique

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Submitted (24-DEC-2001) Toshiaki Katada, University of Tokyo,
Department of Physiological Chemistry, Graduate School of
Pharmaceuttcal Sciences; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033,
Japan (E-mail:katada@mol.f.u-tokyo.ac.jp, Tel:81-3-5841-4750,
Fax:81-3-5841-4751)
                                                                                                                                                                                                                                                                                                                                                      1249 bp
Sequence 77 from Patent W00240715.
AX430295
                                                                                                                                                                                                                            Chalup, M.S., Altus, C.M., Lincoln, S.E.,
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                Patent:
                                                                                                                                                                                                               Molecules for disease detection and treatment
                                                                                                                                                                                                                                                                                           Homo sapiens
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                  Similarity
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   Conservative
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                                                                                                                                                                              : WO 0240715-A 77 23-MAY-2002;
GENOMICS INC (US)
                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte_ID_No: LG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQELLTLETRRNMSLNIDGKRSGKQKRTDRVKGKCTLM"
268 c 239 g 113 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Di-Ras1"
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/tanslation="MPEOSNDYRVVVFGAGGVGKSSLVLRFVKGTFRDTYIPTIEDTY
RQVISCDKSVCTLQITDTTGSHQFPAMQRLSISKGHAFILVFSVTSKQSLEELGFIYK
LIVQIKGSVEDIPVMLVGNKCDETQREVDTREAQAVAQEWKCAFMETSAKMNYNVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   small GTP-binding protein"
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100. .696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Di-rasl"
/note="member of the Ras family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="brain"
/clone_lib="lambda ZAPII human brain cDNA"
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/db_xref="taxon:9606"
/chromosome="19"
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Pred. No. 1.2;
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                                                                                                                                                                                                                               Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA library

construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- $ 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
AX430418
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                                                                                                                                                                                                                                                                                                           28;
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:OCBBF2
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Homo sapiens cDNA FLJ39281 fis, clone OCBBF2011067, highly similar
to Homo sapiens cingulin mRNA.
                   Homo sapiens
Eukaryota;
                                       human
                                                                          AX430418.1
                                                                                                                                   AX430418
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                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="brain"
/clone_lib="0CBBF2"
/dev_stage="fetal"
/note="cloning vector: page 150 c 983 g 40
                                                                                                               200
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Primates;
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                                                                                                                 3061 bp
WO0240715
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Best Local 9
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                    Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanesystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac Anup Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC030660 3391 bp mRNA linear p
Homo sapiens, similar to Rig protein, clone MGC:33391
IMAGE:4814337, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecules for disease detection and treatment Patent: WO 0240715-A 200 23-MAY-2002; INCYTE GENOMICS INC (US)
                                                                                                                                                                                                          prediction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Incyte ID No: LI:332161.1:2000SEP08"
1 840 c 927 g 688 t
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                                                                                                            /db_xref="LocusID:148252"
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                                                                                                                                                   /organism="Homo sapiens"
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84.8%;
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                                                                                                                                                                                                                                                                                                   information can be found
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1 GGGGGATCCATGCCGGAACAGAGTAACGATTAC 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-FEB 1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere. BC41195 (CIT-B-31c16) is currently separated from cosmid R32203 (AC006275) to the left by a sequence gap of approximately 6 kb, and overlaps BAC 103889 (CIT-B-191n6; AC006130) to the right from bases 175,545 to 177,540. Additional map and sequence information are available at: http://www-bio.llnl.gov/bbrp/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lamerdin, J.E., McCready, P.M., Skowronski, E., Viswanathan, V., Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Don, L., Regala, W., Terry, A., Garnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Sanders, C., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine protease gene cluster Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 177540)
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Lamerdin, J.E.
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                            /rpt_family="AluSx"
complement(868. .931)
/rpt_family-"
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LIVQIKGSVEDIPVALVGKKCDETQREVDTYREAQAVAQEWKCAFMETSAKMNYNVKEL
FQELLTLETRRINSLNIDGKRSGKOKRTDRVKGKCTLM"
a 996 c 1016 g 729 t
                                                                                                                                                                                                                                                                                                            complement(1. .144)
/rpt_family="L1MB7"
                                                                                                                                                                                   complement (399.
                                                                                                                                                                                                            /rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                   /note="LLNL clone name:
                                                                                                                                                                                                                                                                                                                                                                                                   /map="19p13.3 between CDC34 and D19S342"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="19"
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	1 -	2441024707 /rpt family="AluSq"	complement(2419124313) /rpt_family="MIR"	complement(2400224172) /rpt_family="MER20"	23136. 23412 23136. 23412 /rpt family="T1MC3"	7.FC_************************************	2269722831 /rpt family="All.Th"	/*E	7 F F F F F F F F F F F F F F F F F F F	complement(2168121811) /rnt family="FLAM C"	\ref \\ref _\ref \ref _\ref \ref _\ref	/IPC_Lamilly MIN complement(2106821332) /rot family="Alisy"	7. PC	/ PC_Funit_Y = NENE complement(20388 20585) /rnt family="MER2O"	rrame: 1, quality: good, score: 53.000" complement(1995320160)	<pre>complement(1957919692) /note="predicted exon, program: grail2exons_human_1.3,</pre>	complement(1930. 1929) /rpt_family="MER20"	1838018748 /rpt_family="MSTD"	/rpt_family="MLT1F"	1/461 .15200 /rpt_family="MER21B"	1/1/81/4/9 /rpt_family="AluSx"	159891/0/3 /rpt_family="MLT1F"	/rpt_family="(GGAA)n"	/rpt_family="AluSx"	/rpt_family="(GAAA)n" 16575	1613016430 /rpt_family="AluSp" 16433	rouvo	156891500/ /rpt_family="AluJo" 15000	1481215011 /rpt_family="(GGGA)n"	1449/14811 /rpt_family="AluSx"	complement(141/314468) /rpt_family="AluY"	1390614116 /rpt_family="L1MC2"	/rpt_family="L1MB8"	complement(13409: .13457) /rpt_family="L1MD3" /rpt_family="L1MD3"	1301313408 /rpt_family="LTR13"	1296013013 /rpt_family="17R13"

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JOURNAL REFERENCE
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RESULT 8
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                                              ATGCCGGAACAGAGTAACGATTAC
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Castro,A.F. and Quilliam,L.A.
Direct Submission
Submitted (13-SEP-2001) Biochemistry and Molecular
University School of Medicine, 635 Barnhill Drive,
Indianapolis, IN 46202, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Castro, A.F. and Quilliam, L.A. Identification of Rig, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ellis, C.A., Vos, M.D., Howell, H.,
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AY056037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
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24; Conservative
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1. .597
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Primates;
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                                                                                                      Score 24; DB 9;
Pred. No. 3.5;
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Pred. No. 0.
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                                                                                                                                        Strausberg, R.
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ATGCCGGAACAGAGTAACGATTAC
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Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
                                                                                  NIH-MGC Project URL: http://i
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                     Direct Submission
Submitted (21-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1875)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens, :
IMAGE:3029902,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (12-OCT-2001) Dept. of Cardiology, U.T. MD. Anderso
Cancer Center, 1515 Holcombe Blvd-449, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP-binding tumor suppressor
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LIVQIKGSVEDIPVMLYGNKCDETQREVDTREAQAVAQSWKCAFMETSAKMNYNVKEL
FQELLTLETRRNMSLNIDGKRSGKQKRTDRVKGKCTLM"
- 195 g 90 t
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/db_xref="taxon:9606"
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Similar to CG8500
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MGC:2364
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RESULT 10
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                                                                                                                                                                                                                    Submitted (24-DEC-2001) Toshiaki Katada, University of Tokyo, Department of Physiological Chemistry, Graduate School of Pharmaceutical Sciences, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-00 Japan (E-mail:katada@mol.f.u-tokyo.ac.jp, Tel:81-3-5841-4750,
                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2505)
Kontani,K., Ogawa,T., Okai,T., Tada,M. and Katada,T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens mRNA for Di-Ras2, complete cds. AB076889 AB076889.1 GI:21624249
                                                                                                                                                                                                                                                                                                                                                                                                 Kontani,K., Tada,M., Ogawa,T., Okai,T. and Katada,T.
Di-Ras: A Distinct Subgroup of Ras-family GTPases with Unique
                                                                                                                                                                                                     Fax:81-3-5841-4751)
                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                              Biochemical Properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens adult brain cDNA
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Madan, Rachel Dickhoff, Jessica Fahey,
ne, Mark Ketteman and Anuradha Madan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Similar to CG8500 gene product"
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438 c 472 g 447 t
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1. .2505
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/note="Vector: pOTB7"
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                                                                                                                                                                                                                      , Graduate School of Bunkyo-ku, Tokyo 113-0033, .jp, Tel:81-3-5841-4750,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
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AX477382
                                                                                                                                RESULT 12
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Best Local
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AC100691

AC100691

AC100691.1 GI:17048057

HTG; HTGS_PHASE0.

Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX477382
Sequence
AX477382
                                                                                                                                                                                                                                                                                                                                                                                                                         Baughn,M.R., Ding,L., Elliott,V.S., Gandhi,A.R., Gietzen,K.J., Griffin,J.A., Gururajan,R., Hafalia,A.J., Kearney,L., Khan,F.A., Lal,P., Lee,E.A., Lu,D.A., Lu,Y., Nguyen,D.B., Arvizu,C., Ramkumar,J., Tang,Y.T., Thangavelu,K., Thornton,M., Walia,N.K., Warren,B.A., Xu,Y., Yao,M.G. and Yue,H. Intracellular signaling molecules Patent: WO 0231152-A 36 18-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Mammalia; F
Eukaryota; Metazoa;
Mammalia; Eutheria;
                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                              Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX477382.1 GI:22216612
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/protein_id="BAC01116.1"
/protein_id="BAC01116.1"
/db_xref="Ci:21624250"
/translation="MPE0SNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYIPTVEDTY
/translation="MPE0SNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYIPTVEDTY
RQVISCDKSICTLOITDTTGSHOFPAMORLSISKGHAFILVYSITSRQSLEELKPIYE
OICEIKGDVESIPIMLYGNKCDESPSREVQSSBAEALARTWKCAFMETSAKLNHNVKE
LFQELLNLEKRRTVSLQIDGKKSKQQKRKEKLKGKCVIM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="member of the Ras family
small GTP-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Di-ras2"
31. .630
                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 490576CB1"
911 c 960 g 1198 t
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Di-ras2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from Patent
                                                                                                   68052 bp clone RP23-168121,
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92.0%;
 Chordata;
Rodentia;
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Pred. No. 35;
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Pred. No. 36;
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Craniata; Vertebrata; Sciurognathi; Muridae;
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LOW-PASS SEQUENCE
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                                                                                                     HTG 22-NOV-2001 SAMPLING.
   Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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COMMENT
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B. Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Cooke, P., Cooke, P., Cooke, P., Cooke, P., Cooke, P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Cooke, P., Dearellano,K., Gage,D., Galagan,J., Gardyna,S., Cooke, P., Cooke, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johns Jones, C., Kamat, A., Karatas, A., Kells, C., Lakocque, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                            sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                             be
                                                                                                                                                                                                                                                                                                                                                                            the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                             will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 68052)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L15958
Center clone name: 168_I_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                      531 1630:
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                                                                                                                           4819: cr
0 4919: cr
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13 812: gap of
13 1530: contig
                                                6555: gap (
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100 bp

100 pc

100 pc

100 bp

2351: contig of 721

2451: gap of

3179: cr
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                                                                                                                                                                                                                                                   2451:
                                   7390:
                                                                                                        5752:
              υ: gap
8113:
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32794: contig of
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31243 31970: contig of
31971 32070
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37032
37759
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28723 28822:
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18904 19629: contig of
9630 10777
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15631 16358: contig of 1

16359 16458: gap of 1

16459 17174: contig of
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11505 12227: c
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8942
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                                                                                                                                                                                                                                                                                                                                                                                                              .../U: gap of 100 b;
(71 27902: contig of 732 b,
03 28002: gap of 100 b;
13 28722: ccr-'
   36931; con
36931; con
37031; gap of
37758; cc
37858;
                                                               36107: cor
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9041: gap
9758:
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11404: contig of
11504: gap of 1
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                                                                                                                                                                                              33729:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24693:
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                                                                                                                                                                               d94: gap of
33629: contig of
33629: of
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5525: gap of 100 bp
26260: contig of 735 b
5360: gap of 100 bp
27070: contig of 710 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22914: contig of 720 k

3014: gap of 100 bp

23751: contig of 737 k

1851: gap of 100 bp

24593: contig of 742 bp

693: gap of 100 bp

1693: gap of 100 bp

1693: gap of 732 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1151: gap of 1
13873: contig of 1
1973: gap of 1
14702: contig of
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                        humquery@sanger.ac.uk Clone
                                           Submitted (09-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 87845)
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20 41849: contig of 730 bp in 16
50 41949: gap of 100 bp
42683: contig of 734 bp in 16
42683: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Nov 15, 2001 this sequence version replaced gi:15591326. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wit only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is not the entire insert of clone RP11-16P8 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-16P8 is at 1 in this sequence. The true left end of clone RP11-551P18 is at 85846 in this sequence. The true right end of clone RP11-422P15 is at 44164 in this
On Oct 11,
During seq
                                                                              Submitted (10-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA sequence from clone RP: 9q21.33-22.33, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RP11-16P8 is from the library RPCI-11.1 Pleter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
                                                         requests: clonerequest@sanger.ac.uk
                                                                                                                                                Direct Submission
                                                                                                                                                                           Laird, G.
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 AL353619.9 GI:16073639
                                                                                                                                                                                                                                                                                                                                                                                                               AL353619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN THE TEATURE TABLE WITH THEIR SOURCE GATABASES: EM:, EMBL; Sw:, INTREDEDITED TO THE WORMPEP; INFORMATION ON THE WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VECTOR: pBACe3.6
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                                                                                                                                                                                                   (bases 1 to 143299)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="10"
/clone="RP11-16P8"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                           2001
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78.8%;
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                           this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21.8;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
version replaced is compared from
                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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gi:15028633
overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI 10-OCT-2001
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   clones
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ORIGIN
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                                                              REFERENCE
                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                       AC021583/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                  VERSION
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                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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Best Local
                                 AUTHORS
                                                                                    JOURNAL
                                                                                                                 TITLE
                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55609 CATGCCTGAGCAGAGTAACGATTAC 55585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_teature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapp
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
AC021583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP11-563G12 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-563G12 is at 143299 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/HGP/Chr9
RP11-563G12 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                 Homo
                                                                                                                                       Birren, B., Nusbaum, C.
                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                  AC021583.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence. The true left end of clone RP11-61N16 is at 51116 in sequence. The true right end of clone RP11-555F9 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                              karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 143857)
                                                        (bases 1 to 143857)
                                                                                                           sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/clone="RP11-563G12"
/clone_lib="RPCI-11.2"
4147. 4230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Single clone region. Assembly confirmed by restriction digest data."
a 29112 c 29198 g 41367 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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                                                                                                                                                                                                                                                                                                                                                                                       chromosome
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92.0%;
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                                                                                                           and Lander,E.
me 9, clone RP11-1026H23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21.8;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                 143857 bp
                                                                                                                                                                                                                                                                                                                                                                                  9, clone RP11-1026H23, complete sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 29-JUN-2002
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REFERENCE

AUTHORS

TITLE JOURNAL

COMMENT

Submitted (29-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 29, 2002 this sequence version replaced gi:21536044. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Institute/ MIT Center for Genome Research

Center: Whitehead

JOURNAL

Direct Submission

Zembek, L., Zimmer, A. and Zody, M.

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Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazgo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Gage, D., Grand-plerre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lin, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Marthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Nienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travis, N., Trigilio, J., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission

Submitted (21-JUN-2002) Whitehead Institute/MIT Center for Genome Submitted (21-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 143857)

Bairen, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Bairen, B., Shabaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Bairan, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Hagos, B.,
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Choepel,Y., Colangelo,M., Collins,Collymore,A., Cooke,I
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
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Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5759
Center clone name: 1026_H_23
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Search completed: March 23, 2003, 16:00:35 Job time: 264.806 secs

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ALIGNMENTS

RESULT 1 ABQ72525 Human MDDT encoding cDNA SEQ 03-SEP-2002 (first entry) ABQ72525 standard; cDNA; 1249 ID NO BP. 77.

Human; MDDT; disease detection and treatment molecule polynuclectide; proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout; neuroprotective; antirheumatic; antiarthritic; gene; ss. Homo sapiens.

WO200240715-A2

23-MAY-2002.

06-SEP-2001; 2001WO-US27628.

06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; ; 2000US-230505P. ; 2000US-230514P. ; 2000US-230515P. ; 2000US-230517P. ; 2000US-230518P. ; 2000US-230519P.

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                                                                                                                                                                                                                                                    polynucleotide comprising. Oligonucleotides and antibodies are useful for detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a biological sample, for detecting (I) in a sample, and for purifying (I) from a sample. A composition comprising (I), an agonist or antagonist is useful for treating a disease or condition associated with decreased or increased expression of functional MDDT (I) or (II) are useful for diagnosing, treating or preventing disorders associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, and cancer and an autoimmune/inflammatory disorder such as ADDS, Addison's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51231-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds (I) or modulates the activity of (I), and for preparing a polyclonal or monoclonal antibody by hybridoma technology. Nucleic acids (II) (AB072449-AB072700) encoding (I) are useful for screening a compound for effectiveness in altering expression of a target
                                                                                                                      allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis of the schematoid arthritis. (II) are useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuand as hybridisation probes for mapping naturally occurring genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-230595P.
2000US-230596P.
2000US-230599P.
2000US-230865P.
2000US-230986P.
2000US-230989P.
2000US-231163P.
2000US-231163P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lincoln
                                                                          BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JY, Wright RJ, Gietzen D, Liu TF,
Bradley DL, Rohatgi SD, Harris B,
Peralta CH, David MH, Panzer SR, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350-351; 618pp; English.
                                                                      230 A; 436 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wright RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SE,
             75.8%;
84.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Altus CM,
Score 25; DB Pred. No. 0.100; Mismatches
                                                                      355 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dufour
                                                                        228
                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inman RR;
                                                                      T; 0
                                    24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             u TF, rap

B, Roseberry P
                                                                      other;
                                Length 1249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flores V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SW.
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                                                                                                                                               individuals
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06-SEP-2000

06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout;
neuroprotective; antirheumatic; antiarthritic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; MDDT; disease detection and treatment molecule polynucleotide;
proliferative disorder; hepatitis; psoriasis; cancer; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200240715-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ72648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ72648 standard;
                                                                                                                                                                                                                                                                                       INCYTE GENOMICS
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2000US-230515P.
2000US-230518P.
2000US-230519P.
2000US-230599P.
2000US-230599P.
2000US-230599P.
2000US-230599P.
2000US-230610P.
2000US-230659P.
2000US-230865P.
2000US-230865P.
2000US-230865P.
2000US-230988P.
2000US-230988P.
2000US-230988P.
2000US-230988P.
2000US-230988P.
2000US-230951P.
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e.g.

JL;

sclerosis;

Gerstin Momiyama MG, EH, s, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE G, Bradley DL, Rohatgi SD, Harris B, Roseber Peralta CH, David MH, Panzer SR, Flores V, Chen AJ, Lincoln SE, Wright RJ, Chang SC, Altus CM, Au AP, Dufour GE, Inman RR; , Chalup MS, H u TF, Yap PE, I s B, Roseberry i Hillman Dahl CR;

WPI; P-PSDB; 2002-527544/56.

or cell

or

e.g. Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.

Claim 1; Page 414; 618pp; English.

The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51231-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound the specifically binds (I) or modulates the activity of (I), and for preparing a polyclonal or monoclonal antibody by hybridoma technology.

Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for of.

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42

GGGGGATCCATGCCGGAACAGAGTAACGATTAC GCGGGGAAGATGCCGGAACAGAGTAACGATTAC

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Matches

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Conservative

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Indels

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AC AA16
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Best Local
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14-SEP-2000;
19-OCT-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
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                                                Tang
Wang
Zhao
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     WPI;
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                                                                                                                                             (HYSE-)
                                                                                                                                                                                                29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia;
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  2001-442253/47
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                                                                                                                                             HYSEQ INC
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                                                Liu C
Wang Z
Zhou
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                                                                                                                                                                                        2000US-0488725.
2000US-0553317.
2000US-0598042.
2000US-0598042.
2000US-0620312.
2000US-0663450.
2000US-0663191.
2000US-0693036.
2000US-0727344.
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                                        u C,
u P,
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                                                                    Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA;
                                                Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.8%;
84.8%;
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                                                                    Chen R,
Xu C,
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Pred. No. 0
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                                                nen R, Ma Y,
Yu C, Xue AJ,
Drmanac RT;
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0.18;
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                                                                 Qian XB,
Yang Y,
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                                                                    Ren F,
Zhang
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Matches
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Best Local
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                             Human: nootropic: immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS: Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI59052 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                           14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                26-DEC-2000;
                                                                                                                                                                                                         26-JUL-2001
                                                                                                                                                                                                                                  WO200153312-A1
                                                                                                                                                                                                                                                                                                   chemokinetic;
                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 1255.
                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification
                                 (HYSE-)
                                                                                                                                                                                                                                                                                      leukaemia; ss
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23; Conservative
                                     HYSEQ
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                                                            2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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                                                                                                                                           2000US-0488725
2000US-0552317
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92.0%;
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                                                                                                                                                                                                                                                                                                  inflammation;
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Liu Wang

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Asundi V, Wehrman T,

Chen Xu (

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Ma Xue

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Qian XB, Yang Y,

Zhang

Wang

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                    Human; intracellular signalling; INTSIG-16; gene therapy; nausea; asthma; Crohn's disease; keratosis; cell proliferative disorder; Grave's disease; arteriosclerosis; hepatitis; leukaemia; autoimmune disorder; meningitis; acquired immunedeficiency syndrome; AIDS; allergy; dermatitis; psoriasis; Hashimoto's thyroiditis; neurological disorder; developmental disorder; gastrointestinal disorder; reproductive disorder; nootropic; antiemetic; psoriasis; disease; dementia; Creutifeldt_Jacob disease; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                               gynaecological; gene; ss
                                                                                                                                                                                                                                                                                                                                                                     Human intracellular signalling (INTSIG-16) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1108 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
             WO200231152-A2
                                                                   mat_peptide
                                                                                               sig_peptide
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                           antiinflammatory; anaemia; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD37605 standard; cDNA; 4167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acids and polypeptides, useful for treating disorders as central nervous system injuries -
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23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for receptor activity, arthritis and inflammation, leukaemias and
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260..757
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161..259
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                                                                                                                                                      Location/Qualifiers
                                      'product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 A;
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92.0%;
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                                                                                                                                                                                                                            cerebroprotective;
                                                                                                            "Human
                                      "Mature INTSIG-16 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21.8;
Pred. No. 4.
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                                                                                                            INSIG-16 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patent did not
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                                                                                                                                                                                                                                           immunosuppressive;
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                                                                                                                                                                                                                            antibacterial;
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Best Local :
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30-OCT-2000;
15-NOV-2000;
22-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder e.g. keratosis, arteriosclerosis, hepatitis, psoriasis, leukaemia; autoimmune disorders e.g. AIDS, allergies, anaemia, asthma, Crohn's disease, dermatitis, Graves' disease, Hashimoto's thyroiditis; neurological disorders e.g. Alzheimer's disease, dementia, meningitis, Creutzfeldt-Jacob disease; gastrointestinal disorders e.g. nausea, reproductive disorders e.g. menstrual disorders, ectopic pregnancy and cancer of the breast and developmental disorders. The present sequence
                                                                                             vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                1981/c
AAI91981 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated intracellular signalling (INTSIG) polypeptide or a biologically active or immunogenic fragment of INTSIG INTSIG is also useful for preparing a polyclonal or monoclonal antibody by hybridoma technology. INTSIG gene is useful in gene therapy. INTSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 91; Page 171-172; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal and
                                        WO200164835-A2
                                                                 Homo sapiens
                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                              Human polynucleotide SEQ ID NO 12041.
                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4167 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by hybridoma technology. INTSIG gene is useful in gene therapy. INTSIG is useful for treating or preventing disorders such as cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel intracellular signaling polypeptide useful for treating preventing cell proliferative, autoimmune, neurological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
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Yue H;
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DB; AAE23389.
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23; Conserv
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                                                                                           system
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTSIG-16 cDNA.
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Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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2000US-244723P.
2000US-249402P.
2000US-252622P.
                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                             1098 A; 911 C;
                                                                                                                                                                                                                                                 CDNA; 402
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92.0%;
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Arvizu C,
Walia NK,
                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                  Score 21.8;
Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                             960 G; 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warren BA,
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Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                                                     DB
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FA, Lal P,
Nar J, Tang Y
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YT;
                                                                                                                                                                                                                                                                                                                                                                                                      4167;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The prolynecleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and may be useful in the diagnosis and/or treatment of capacity levels and levels and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AA013910) that exhibit activity elating to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 12041; 1399pp + Sequence Listing; English.
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18-MAY-2000;
                                                                 Dumas Milne Edwards J,
                                                                                                                                                                                                        21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                     2000-500381/45
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2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein 5'
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75.8%;
                                                                 Duclert
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                                                                 Giordano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC78063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAS o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC78063 standard; cDNA; 3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                    P-PSDB; AAB43854
                                                                                                                        WPI; 2000-587533/55
                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200055350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemostatic; thrombolytic; neurological disease; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer associated gene sequence SEQ ID NO:457
                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                               12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGGATCCATGCCGGAACAGAGTAACGATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCAGCTCCATGCTGGAACAGAGTAGGGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 BP; 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                               99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2297; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      graft versus host disease; organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%;
75.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 105 C; 145 G; 106 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 20.2; [; Pred. No. 21; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing $e.g.\ cancer$ -

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating
 Claim 1; SEQ
                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirhemmatic; antiarthritic;
                                                                                                                    WPI; 2001-639362/73.
P-PSDB; ABG30214.
                                                                                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002
                                  biodiversity
                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                    11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #30205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS94401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS94401 standard; cDNA; 4011 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                    Drmanac RT,
                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGGATCCATGCCGGAACAGAGTAACGATTAC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3249
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                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
 ij
                                                                                                                                                                                                                                    2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 900 A; 711 C;
No 30205; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.2%;
75.8%;
                                                                                                                                                                 Tang YT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20.2;
Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                 SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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The present invention provides the protein and coding sequences of secretory acid phosphatase from the white lupine which combines to surface of plant roots. The sequences are useful for producing plan

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RESULT 10
AAF81507/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide (II) sequences. (I) is useful as hybridisation probes,

compolymerase chain reaction (PCR) primers, oligomers, and for chromosome

cand gene mapping, and in recombinant production of (II). The

compolynucleotides are also used in diagnostics as expressed sequence tags

compolynucleotides are also used in diagnostics as expressed sequence tags

compolynucleotides are also used in diagnostics as expressed sequence tags

compolynucleotides are also used in diagnostics as expressed sequence tags

compolynucleotides are also used in diagnostics as expressed sequence and as

component (II) is useful for generating antibodies against it, detecting or

component (II) and (II) and (II) are useful in medical

component (II) and (II) and (II) are useful for treating

component (II) are useful for treating

component (II) and (II) are useful for treating

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on D amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention of the Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                   Claim 1; Page 9-11; 17pp; Japanese
                                                                                                                               Secretory acid phosphatase
                                                                                                                                                                                                                                                                                                                                      07-JAN-2000; 2000JP-0001442.
                                                                                                                                                                                                                                                                                                                                                                                  06-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                         JP2001029085-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White lupine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -507/c
AAF81507 standard; DNA; 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3099 GGCAGCTCCATGCTGGAACAGAGTAGGGAATTC 3131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4011 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                (MITA ) MITSUI CHEM INC.
                                                                                                                                                                                                                                                                                            18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lupinus albus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White lupine secretory acid phosphatase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF81507;
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                                                                                                                                                                               2001-221499/23
DB; AAB74496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGGATCCATGCCGGAACAGAGTAACGATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secretory acid phosphatase;
                                                                                                                                                                                                                                                                                            99JP-0137273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "secretory acid phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1075 A; 910 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%;
75.8%;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 953 G; 1073
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G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           root; phosphor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                               cc signalling in taste cells, by contacting the compound with a eukaryotic channel subunit (TC-TCS), and determining a functional effect of the cchannel subunit (TC-TCS), and determining a functional effect of the ccompound upon a transmembrane ion flux of a predetermined ion, clientifying a compound that modulates taste signalling in taste cells. (M1) is useful for identifying a compound that modulates taste signalling cc in taste cells, for identifying a compound that binds to a taste cell cc epselfic ion channel subunit and for modulating taste signalling in taste cells of a mammal, in particular a human. Modulators identified by (M1) cc e.g. as additives to food or medicine so that the food or medicine taste, cc different to the subject who ingests it. Bitter medicines can be made to cuseful for pharmacological and genetic modulation of taste signalling cuseful for pharmacological and genetic modulation of taste signalling completes for medical sets that the food or medicines are useful for pharmacological and genetic modulation of taste signalling completes for medical sets that the food or mammalian that the food or medicine taste signalling completes for medical sets that the food or medicine taste signalling completes for medical sets that the food or medicine taste signalling complete for medical sets that the food or medicine taste signalling complete for medical sets that the food or medicine taste signalling complete for medical sets that the food or medicine taste signalling complete for medical sets that the food or medicine taste signalling complete for medical sets that the food or medicine taste signalling complete for medical sets to the food or medicine taste signalling complete for medical sets of the food or medicine taste signalling complete for medical sets of the food or medicine taste signalling complete for medical sets of the food or medicine taste signal sets of the food or medicine taste signal sets of the food or medicine taste signal sets of the food or medicine taste components t
                       Query Match
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  Best Local Similarity
                                                                                                         pathways. The taste modulations can be writer, The present sequence is that of subjects for modulation of taste in vivo. The present sequence is that of the mouse genomic region containing the ltrpc5 gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying modulators of taste signaling in taste cells for use in food and pharmaceutical industries to customize and regulate taste, by determining effect of the compound on a taste cell-specific ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-2000;
21-DEC-2001;
                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying (M1) a compound that modulates taste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 64-207; 306pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zuker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; ltrpc5; taste; cell signalling; TC-ICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse genomic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN85733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN85733 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1702 GGGGACTCATGCCGGAGATGAGGAACGATAA 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2187 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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2001US-0026188.
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                                                                          BP;
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                                                                        64808 A; 61913 C; 61498 G; 61236 T; 32 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ion channel subunit; gene; ds.
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77.4%;
58.8%;
79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing the ltrpc5 gene SEQ ID NO
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Score 19.4; DB 24
Pred. No. 1.1e+02;
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                       DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        food; pharmaceutical;
                    Length 249487;
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RESULT
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                                           or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC7844 AAC78457 and AAB44240 represent sequences used in the exemplification
                                                                                                                                                                                               dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating o ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activations.
                                                                                                                                                                                                                                                                                                           include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriatic; antiangiogenic; therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated gene
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                                                                                                                                                                                                                                                                                                                                                                 in AAB43398 to AAB44239. The proteins can have activities based on tissues and cells the genes are expressed in Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 803-804; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB43630
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                                  present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated nucleic
l for treating or
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                                                                                                                                                                                                                                                                                                                                                                                                       AAC78448 encode the human cancer associated proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids comprising sequences encoding peptides diagnosing e.g. cancer \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening; ss
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                                                                                                            disease and
                                                       AAC78449 to
ication of
                                                                                                                                                                                                   activating
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RESULT 13
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Best Local
                               encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can used as nutritional sources or supplements and in the screening
                                                             be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it
                                                                                                                                          The present sequence is one of 251 novel human polynuc expressed in the bone marrow. The polynucleotide and t polyneptide encoded by it are useful in the treatment
                                                                                                                                                                                             Claim
                                                                                                                                                                                                              03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                            25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow cDNA,
                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                     Zhao
                                                                                                                                                                                                                                                                                               Ren F,
                                                                                                                                                                                                                                                                                                            Ford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone
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                                                                                                                                     immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive;
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                                                                                                                                                                                                                                                                                       JE, Wang
                                                                                                                                                                                                                                                             2001-488707/53.
                                                                                                                                                                                                                                                                                    Q
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
                                                                                                                                deficiencies and disorders. The deficiencies and disorders may
                                                                                                                                                                                                                                                    AAM00978.
                                                                                                                                                                                                                                                                                                                                HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                      compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                   Zhou P,
                                                                                                                                                                                                                                                                                                           Boyle BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e marrow; antiinflammatory; cytostatic; neuroprotective;
antibacterial; antifungal; anti-HIV; haemostatic;
ressive; gene therapy; cytokine cell proliferation;
rentiation modulator; immune disorder; infection; cancer
                                                                                                                                                                                                                                                                                                                                                    2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0250583.
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                                                                                                                                                                                                                                                                                              Werhman T,
                     as
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                                                                                                                                                                                                                                                                                     Drmanac RT;
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75.0%;
                     potential drugs.
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                                               diagnosis and/or prognosis of one
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Xue /
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ue AJ, Yang
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                                                                                                                                                                    polynucleotides
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g Y, Zhai
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                              the screening
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                                                                                                                                                                                                                                                                                              Zhang
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ng J;
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Sequence

5201

BP;

1460

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Sequence

5294

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Best Local S
Matches 24
                                                            expressed in the bone marrow. The polynucleotides and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the proton it encodes is useful for the diagnosis and/or prognosis of one used as nutritional sources or supplements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4476
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200153453-A2
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Wang
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                                                compounds
                                                                                                                                                                                                                                                                                                                                                                                                   Page 422-423;
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ang J, Wer
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2000US-0552317
2000US-0598042
2000US-0620312
2000US-0623450
2000US-0662191
2000US-0663195
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Werhman T,
                                                as
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                                                potential drugs.
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ue AJ, Yang
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Y, z
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RESULT 15
AAS74120/c
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II) The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO at fire intensity from WIPO.
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Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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P-PSDB; ABG09933.
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23-AUG-2000; 2000US-0649167.
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                              ftp.wipo.int/pub/published_pct_sequences
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24; Conservative
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Query Match

Sequence 5396 BP; 1623 A; 1085 C; 1157 G;

58.2%;

Score 19.2;

DB

Length 5396;

1531 T; 0 other; 23;

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Best Local Similarity 75.0 Matches 24; Conservative
75.0%;
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Search completed: March 23, 2003, 15:19:51 Job time : 113.871 secs

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Post-processing: Minimum Match 0%
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Perfect score:
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Maximum DB seq length: 2000000000
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gb_pot: *
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 AY056037

LOCUS	AY056037 597 bp mRNA linear PRI 24-JUL-2002
DEFINITION	Homo sapiens Rig protein mRNA, complete cds.
ACCESSION	AY056037
VERSION	AY056037.1 GI:16555333
KEYWORDS	
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 597)
AUTHORS	Ellis, C.A., Vos, M.D., Howell, H., Vallecorsa, T., Fults, D.W. and
ም/ተ	Clark,G.J. Rig is a novel Ras-related protein and potential neural tumor
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Pred. No. is the number of results predicted by chance to have a

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Castro, A.F. and Quilliam, L.A.
Direct Submission
Submitted (13-SEP-2001) Biochemistry and Molecular Biology,
University School of Medicine, 635 Barnhill Drive, MS-4053,
Indianapolis, IN 46202, USA
Location/Qualifiers
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3 (bases 1
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LIVQIKGSVEDIPVMLVGNKCDETQREVDTREAQAVAQEWKCAFMETSAKMNYNVKEL
FQELLTHLETRRNMSLNIDGKRSGKGKTTDRVKGKCTLM"
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/chromosome="19"
/map="19p13.3"
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/note="derived from dbEST AI497811"
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Gong, L. and Wu, K.
Molecular cloning of GBTS1, a novel gene encoding try of the constraint of the con
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Submitted (12-OCT-2001) Dept.
Cancer Center, 1515 Holcombe
Location/Qualifiers
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X 77030, USA
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    Matches 596;
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AB076888
AB076888.1
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-DEC-2001) Toshiaki Katada, University of Tokyo, Department of Physiological Chemistry, Graduate School of Pharmaceutical Sciences; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:Katada@mol.f.u-tokyo.ac.jp, Tel:81-3-5841-4750,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 774)
Kontani,K., Ogawa,T., Okai,T.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kontani,K., Tada,M., Ogawa,T., Okai,T. and Katada,T.
Di-Ras: A Distinct Subgroup of Ras-family GTPases with Unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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    Conservative
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                                                                   /Protein_id="BAC01115.1"
/Protein_id="BAC01115.1"
/db_xref="GI:21624248"
/db_xref="GI:21624248"
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LIVQIKGSVEDIPVMLVGNKCDETQREVDTREAQAVAQEWKCAFMETSAKMNYNVKEL
FQELLTLETRRNMSLNIDGKRSGKGKRTDRVKGKCTLM"
268 c 239 g 113 t
                                                                                                                                                                                       /note="member of the Ras fi
small GTP-binding protein"
                                                                                                                                                                                                                                 /gene="Di-rasl"
100. .696
                                                                                                                                                                                                                                                                     /tissue_type="brain"
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/dev_stage="adult"
                                                                                                                                                               /product="Di-Rasl"
                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                              /chromosome="19"
                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        'organism="Homo sapiens"
                99
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 : Score 595.4;
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               CGCTCCGGGAAGCAGAAGAGGGACAGACCGCGTCAAGGGCAAATGCACCCTCATGTGA 597
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TITLE JOURNAL REFERENCE VERSION KEYWORDS REFERENCE SOURCE ACCESSION DEFINITION rocus AUTHORS TITLE AUTHORS ORGANISM Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishil,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T. NEDO human CDNA sequencing project 2 (bases 1 to 2827)
Isogai,T. and Yamamoto,J.
Direct Submission Unpublished Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria; oligo capping; fis (full insert sequence).
Homo sapiens fetal brain cDNA to mRNA, clone_lib:OCBBF2 2827 bp Homo sapiens cDNA FLJ39281 fis, to Homo sapiens cingulin mRNA. AK096600 clone:OCBBF2011067 AK096600.1 GI:21756131 AK096600 Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. mRNA linear clone OCBBF2011067, PRI 15-JUL-2002 highly similar

JOURNAL

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Fax:81-438-52-3986)

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VERSION
KEYWORDS
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BC030660
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BC030660.1 GI:21040534
                                                                       Homo sapiens,
IMAGE: 4814337,
                                                                                                     BC030660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
sapiens.
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/note="cloning vector:
750 c 983 g (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="brain"
/clone_lib="OCBBF2"
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/db_xref="taxon:9606"
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                                                                                     similar to Rig protein, clone
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596; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 46 Row: e Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NH
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prediction.
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madan, Stephanie Rodrigues,
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RQVISCDKSVCTLQITDTTGSHQFPAMQRLSISKGHAFILVFSVTSKQSLEELGPIYK
LIVQIKGSVEDIPVMLVGNKCDETQREVDTREAQAVAQEWKCAFMETSAKMNYNVKEL
FQELLTLETRRNMSLNIDGKRSGKQKRTDRVKGKCTLM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript'
138. .734
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/protein_id="AAH30660.1"
/db_xref="GI:21040535"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
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/db_xref="LocusID:148252"
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                                                                                                                                                                                                                                                                                                                                                 Direct Submission

Submitted (07-FEB-1999) Joint Genome Institute, Lawrence Livermore Submitted (07-FEB-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere. BC41195 (CIT-B-31c16) is currently separated from cosmid R32203 (AC006275) to the left by a sequence gap of approximately 6 kb, and overlaps BAC 102889 (CIT-B-191n6; AC006130) to the right from bases 175,545 to 177,540. Additional map and sequence information are available at: http://www-bio.linl.gov/bbrp/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu,S., Attix,C., Andreise,T., Trankheim,M., Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G., Kronmiller,B., Arellano,A., Sanders,C., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and Carrano,A.V.

Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC006538 177540 bp
Homo sapiens chromosome 19, BAC
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1 (bases 1 to 177540)

Lamerdin, J.E., McCready, P.M., Skowronski, E., Viswanathan, V.,
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                                                 complement(399
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/rpt_family="L1MC/D"
  complement(438. .738)
                                                                                                                                                                                                /map="19p13.3 between CDC34 and D19S342"
/clone="CIT-B-31c16"
/clone_lib="Cal tech CIT-B BAC library"
                                                                        /rpt_family="AluJo"
                                                                                                                                                                        /note="LLNL clone name: BC41195"
                                                                                                                                                                                                                                                                              /chromosome="19"
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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1175. .1365
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frame: 2, quality: good, score: 57.000"
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10631. .10756
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13013. .13408
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                                                                                          Molecules for disease detection and treatment
Patent: WO 0240711-A 77 23-MAY-2002;
INCYTE GENOMICS INC (US)
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: LG:
436 c 355 g 22
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complement(24739. .24926)
/rpt_family="MER58A"
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Pred. No. 2.2e-82;
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Sequence 20
AX430418
AX430418.1
                                                                                                        Chalup,M.S., Altus,C.M., Lincoln,S.E., Dufour,G. Molecules for disease detection and treatment Patent: WO 0240715-A 200 23-MAY-2002; INCYTE GENOMICS INC (US)
                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: LI:
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                                                        Gong,L.

Direct Submission
Direct Submission
Cancer Center, 1515 Holcombe BJ
Location/Qualifiers
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Gong, L. and Wu, K.
Molecular cloning of
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  /gene="Gbts1"
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                      /db_xref="taxon:10090"
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                                         organism="Mus musculus"/strain="129/SvJ"
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GTP-binding
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Bukaryota; Metazoa; Chordata; Craniata; Verte

Mammalia; Eutheria; Rodentia; Sciurognathi; J

1 (bases 1 to 126901)

Kim,J., Shaull,S., Yao,Z., Andrews,G.K. and

Mus musculus BAC Clone mgs1-257j2
                                                                                                               11 Similarity 89.9
537; Conservative
                                                                                                                                                                      Mus musculus chromosome 10 clone mgs1-257j2
DRAFT SEQUENCE, 5 unordered niccon
                                                                                                            HTG; HTGS_PH house mouse.
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/codon_start=1
/product="small GTP-binding tumor suppressor 1"
/product="small GTP-binding tumor suppressor 1"
/protein_id="aall7967.1"
/db_xref="GI:16508174"
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RQVISCDKSVCTLQITDTTGSHQFPAMQRLSISKGHAFILVFSVTSKQSLDELSPIYK
LIVQIKGSVEDLFIMLVGNKCDETQREVHTREAQAVAQEWKCAFMETSAKMNYNVKEL
FQELLTLETRRSVSLSVDGKRSSKQKRADRIKGKCALM"
166 c 194 g 99 t
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Pred. No. 1.7e-67;
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129/SvJ,
                                                           Murinae;
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SvJ, WORKING
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Best Local
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TACAAGCTCATCGTGCAGATCAAGGGCAGCGTGGAGGACATCCCCGTGATGCTCGTGGGC
                                                     GCCTTCATCCTGGTGTTCTCCGTCACCAGCAGCAGTCGCTGGAGGAGCTGGGGGCCCATC
                                                                                                           GACACCACCGGCAGCCACCAGTTCCCGGCCATGCAGCGGCTGTCCATCTCCAAGGGCCAC
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                                      GCCTTTATCCTGGTGTTCTCGGTGACCAGCAAGCAGTCGCTGGATGAGCTGAGCCCCATC
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OK 73019, USA
3 (bases 1 to 126901)
Kim,J., Shaull,S., Yao,Z., Andrews,G.K.
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The University Of Oklahoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OK 73019, USA On Aug 14, 2002 this sequence version replaced gi:21955024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-AUG-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/clone_lib="Genome Systems mouse
and II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="129/SvJ"
/db_xref="taxon:10090"
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7855: gap of unknown length
29448: contig of 21593 bp in length
29548: gap of unknown length
58825: contig of 29277 bp in length
58925: gap of unknown length
68918: contig of 30693 bp in length
89718: gap of unknown length
126901: contig of 37183 bp in length.
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89.9%;
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                                                                                                                                                                                                                                     Consensus quality: 195092 bases at least Q40
Consensus quality: 198903 bases at least Q30
Consensus quality: 199767 bases at least Q20
Estimated insert size: 209000; agarose-fp estimation
Estimated insert size: 200820; sum-of-contigs estimation
Quality coverage: 12.12 in Q20 bases; agarose-fp estimation
Quality coverage: 12.62 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. Gaps between the contigs
* are represented as runs of N. The order of the places
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center Project Name: 1763831
Center clone name: RPCI-23_70D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jul 18, 2000 this sequence version replaced gi:8810433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 201320)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Summary Statistics
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Rodentia;
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                                                                                                               by t
                                                                                                                                                      is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced
the finished sequence as soon as it is available and a accession number will be preserved.

1 14454: contig of 14454 bp in length
14455 14554: gap of unknown length
1455 15360: contig of 806 bp in length
15361 15460: gap of unknown length
15461 17163: contig of 1703 bp in length
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                                                                           TTCCAGGAGCTGCTGACGCTGGAGACGCGCCGGAACATGAGCCTCAACATCGACGGCAAG
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CGCTCCAGCAAGCAGAAGAGGGCTGACCGCATCAAGGGCCAAGTGCGCGCTCATGTGA 114503
                             CGCTCCGGGAAGCAGAAGAGGACAGACCGCGTCAAGGGCAAATGCACCCTCATGTGA 597
                                                           TTCCAGGAGCTGCTGACGCTCGAGACGCGCCGGAGCGTCAGCCTCAGCGTGGACGGCAAA 114560
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/db_xref="taxon:10090"
/clone="RP23-70D7"
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132272: contig of 28815 bp in length
132372: gap of unknown length
135372: contig of 3355 bp in length
135727: contig of 3355 bp in length
135827: gap of unknown length
196460: contig of 60633 bp in length
196560: gap of unknown length
200718: contig of 4158 bp in length
200818: gap of unknown length
201320: contig of 502 bp in length.
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Pred. No. 6e-68;
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bouck, J., Bowle, S., Brieva, M., Brown, M., Brown, M., Brown, M., Brown, M., Brown, M., Bryant, N.P., Blukett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorn, S.R., David, R., David, R., David, M.C., Davy, Carroll, L., Dederich, D.A., David, M.C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferreguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Halle, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Ja, Y., Johnson, R., Jolivet, S., Joudah, S., Karison, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karison, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karison, E., Kelly, S., Hantin, R., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karison, E., Kelly, S., Martin, R., Leal, B., Lewis, L.C., Lewis, L., Li, J., Liu, W., Loulseged, H., Lozado, R., Ja, R., Martin, R., Martindele, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Myuen, A., Nguyen, N., Nickerson, E., McLeod, M.P., Meador, M., Myuen, N., Merzker, M., Manner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Meser, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtarl, N., Sisson, I., Sodergren, E., Sonalker, T., Sparks, A., Stanley, H., Stone, H., Mann, G., Welle, M., Welle, M., Marting, R., Wang, O., Welle, M., Welle, M., Welle, M., Mann, S., Welson, D., Wang, O., Wang, C., Walle, K., Wang, O., W
                                                                                                                                                 Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced gi:17973594.
                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-NOV-2001) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 153386)
                                                                                                                                                                                                                                                                                                                                            Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley, K.C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T. Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny, D.M., Adams
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                                                                        Center: Baylor College of Medicine Center code: BCM
Web site: http://www.hgsc.bcm.
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                       Genome Center
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, Banks,T.,
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 63 contigs. The true order of the places

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GICZ
Center clone name: CH230-192M3
Center summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap: version 0.990329 Consensus quality: 83570 bases at least Q40 Consensus quality: 86559 bases at least Q30 Consensus quality: 88900 bases at least Q20
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                        Custom primer used for sequencing
( 5' end primer [CTTCTGCTCTAAAAGCTGCG];
3' end primer [CGACCTGCAGCTCGAGCACA] ).
                                                                                                                                                                                                                                                                                 sequence.
                                                                                                             Lab host:
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TTCCAGGAGCTGCTGACGCTGGAGACGCGCCGGAACATGAGCCTCAACATCGACGGCAAG
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                   Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashienh.go.jp, URL:http://www.nih.go.jp/yoken/genebank/.Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                  2 (bases 1 to 4412) Hashimoto, K., Osada,
                                                                                                                                                                                                                                                                                 Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K. Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca fascicularis
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Macaca fascicularis adult male frontal lobe left cDNA to mRNA, clone_lib:macaque brain cDNA library QflA clone:QflA-13004.
                                                                                                                             Submitted (11-JUN-2001) Katsuyuki Hashimoto, National Institute
                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                 Unpublished
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                        Homo sapiens, IMAGE:3029902,
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/protein_i(="BAB60730.1"
/protein_i(="BAB60730.1"
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/translation="MPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYIPTVEDTY
RQVISCDKSICTLQITDTTGSHQFPANGCLSISKGHAFILWYSITSRQSLEELKPIYE
GICEIKGDMESIPIMLVGNKCDESPESREVQSSEABALARTWKCAFMETSAKLNHNVKE
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/clone_lib="macaque b
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/clone="QflA-13004"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 3 Row: p Column: 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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RQVISCDKSICTLQITDTTGSHOFPAMORLSISKGHAFILVYSTSRQSLEELKPIYE
QICEIKODVESIPIMLVGNKCDESPSREVQSSEAEALARTWKCAFMETSAKLNHNVKE
LFQELLNLEKRRYVSLQIDGKKSKQQKKKEKLKGKCVIM"

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/protein_id="AAH08065.1"
/db_xref="GI:14165525"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Ovary, adenocarcinoma"
/clone_lib="NIH_MGC_9"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:2364 IMAGE:3029902"
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Submitted (24-DBC-2001) Toshiaki Katada, University of Tokyo,
Department of Physiological Chemistry, Graduate School of
Pharmaceutical Sciences; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033,
Japan (E-mail:katada@mol.f.u-tokyo.ac.jp, Tel:81-3-5841-4750,
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Homo sapiens mRNA for Di-Ras2,
AB076889
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Kontani,K., Ogawa,T., Okai,T.,
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small GTP-binding protein"
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SUMMARIES

Score Query Match 92.4 92.4 92.4 92.4 92.4 10960 126901 176340 177540 180544 201320 Length 1249 1574 1624 1698 1698 2763 2827 3061 3391 6710 7701 1494 1545 1563 1566 1566 1567 1568 1568 1568 1568 1568 1568 DВ 19691 ဖ ဖ 10 AX430295 AX630295 AB008423 0 AB008423 0 RATCYPDB2 2 CCU56652 AK096600 AX430418 BC030660 CAJ10321 1 RSIID2G AB005869 AC001518 AC107527 AC075816 AC107527 AC073816 AF180424 AF315501 AF180424 AF315501 AF320123 AF255672 HSP450 AX411044 AF31647 E10867 E10868 E10869 E10869 HSP450IID AR084365 AR084374 HSDB1 HUMCYPDB1 A20907 AR084372 AR084373 AR084373 MFU38218 E15820 AB076888 AY056037 Ħ AX430295 Sequence AX430295 Sequence AB008423 Rattus no M16655 Rat cytochr M22330 Rat cytochr M22330 Rat cytochr M22330 Rat cytochr M22330 Rat cytochr M2330 Rat cytochr M2330 Rat cytochr M250562 Caulobact AX430418 Sequence BC030660 Homo sapi AX430418 Sequence BC030660 Homo sapi AX430418 Sequence BC0306638 Homo sapi AC107527 Rattus no AC006538 Homo sapi AC107315 Human mRNA AX41044 Sequence E10647 Human mRNA AX41044 Sequence E10870 cDNA encodi E10869 cDNA encodi E10869 cDNA encodi E10870 cDNA encodi E10871 Human mRNA AX41044 Sequence AR084374 Sequence AR084375 Sequence AR084375 Sequence AR084375 Sequence AR084375 Sequence AY059641 Homo AY059640 Mus AX195173 Sequence AB076888 Homo sapi Description

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Proc. Natl.
12107278
                                                                                                                             Submitted (12-OCT-2001) Dept. of Cardiology, U. Cancer Center, 1515 Holcombe Blvd-449, Houston,
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Castro,A.F. and Quilliam,L.A.
Identification of Rig, a nove
with NOEY2 and Rap
                                                                                                                                                                                  Gong, L.
                                                                                                                                                                                                                                          Gong, L. and Wu, K.
Molecular cloning of GBTS1, a
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 597)
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Eukaryota; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-SEP-2001) Biochemistry and Molecular Biology, University School of Medicine, 635 Barnhill Drive, MS-4053, Indianapolis, IN 46202, USA
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Castro, A.F. and Quilliam, L.A.
Direct Submission
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LIVQIKGSVEDIPVMLVGKKDETQREVDTREAQAVAQEWKCAFMETSAKMNYNVKEL
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a 178 c 195 g 90 t
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                                                              /organism="Homo sapiens"
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                                                                                                   Location/Qualifiers
1. .597
                                                   'chromosome="19"
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Mammalla; Eutheria; Rodentia;
1 (bases 1 to 597)
Gong, L. and Wu, K.
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Sequence
AX430295
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              Chalup, M.S.,
                                                                   Homo sapiens
                                                                                   numan
                                                                                                             AX430295.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kontani,K., Ogawa,T., Okai,T.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemical Properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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 Molecules for disease detection and treatment
                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax:81-3-5841-4751)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                       77
                                                                                                                                                                                                                                                                                                                                                /protein_id="BAC01115.1"
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/db_xref="G1:21624248"
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LIVQIKGSVEDIPVMLVGNKCDETQREVDTREAQAVAQEWKCAFMETSAKMNYNVKEL
FQELLTLETRRNMSLAIDGKRSGKQKRTDRVKGKCTLM"

268 c 239 g 113 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       small GTP-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="brain"
/clone_lib="lambda Z
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="member of the Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Di-ras1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="19p13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                            product="Di-Ras1"
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                                                                                                           GI:21655659
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               Altus, C.M.,
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                                                                                                                                                                                                                                                                                           92.4%;
95.2%;
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Primates;
                                        Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                               0;
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Pred. No. 53;
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              Lincoln, S.E.,
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              Dufour, G.E.
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                                         Homo
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Direct Submission
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                                                                                                                                                                              /product="CYP2D2"
                                                                                                                                                                                                                       /gene="CYP2D2"
                                                                                                                                                                                                                                              /gene="CYP2D2"
                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                             /codon_start=]
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and their catalytic specificity Arch. Biochem. Biophys. (1997) In 2 (bases 1 to 1574)
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Expression of four rat CYP2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (strain:Sprague-Dawley) 7 tissue_lib:cDNA cDNA to mRNA.
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GHLCDTFAKEAEHPFNPSILLSKAVSNVIASLYVYARRFEYEDPFFNRHLKTLKESFGE
DTGFMAEVLNALPILLQIFGLFGKVFPKLNSFIALVDKMLIEHKKSWDPAQPPRDMTD
AFLAEMQKAKGNPESSFNDENLRLVVIDLFMAGMVTTSTTLSWALLLMILHPDVQRRV
                         HEEIDEVIGQVRRPEMADQARMPFTNAVIHEVQRFADIVPTNIPHMTSRDIKFQGFLI
PKGTTLIPNLSSVLKDETVWEKPLRFHPEHFLDAQGNFVKHEAFMPFSAGRRACLGEP
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/db_xref="Incyte ID No: LG:389870.1:2000SEP08"
/note="Incyte ID No: LG:389870.1:2000SEP08"
436 c 355 g 228 t
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/tissue_lib="cDNA"
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/db_xref="taxon:10116"
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1. .1249
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                                                                                                                                                                                                                                                                                                                                                note="CYP2D cytochrome P450 isoform"
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for CYP2D2,
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Murinae;
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KEYWORDS
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                        Rat cytochrome P450
M22330
M22330.1 GI:203823
  cytochrome P450.
Rat (Sprague-Dav
                                                                                                                                                                                                                               Unreported.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1624)
Gonzalez, F.J., Matsunaga, T., Nagata, K., Meyer, U.A., Pastewka, J., Kozak, C.A., Gillette, J., Gelboin, H.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M16655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subfamily, regulation, chromosomal mapping, of the DA rat polymorphism DNA 6 (2), 149-161 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hardwick, J.P.
Debrisoguine 4-hydroxylase: characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat (Sprague-Dawley, clone pP450db2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytochrome P450; debrisoquine 4-hydroxylase. Rat (Sprague-Dawley, 8 week old) liver microsome,
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                                                                                                                                                                                           Similarity
  (Sprague-Dawley,
                                                                                                                                                                                                                                            347
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                               CTANS 1 a tion = "MGLLIGDDLMAVVIFTAIFLLLVDLVHRHKFWTAHYPPGPVPLP
GGGNLLOVDFENNPYSLYKLRSRYGDVESLQIAWKPVVVIGLKAVRELLVTVGEDTA
DRPLLPTYNHLOYGNKSKGVVLAPYGEBMREGNRFSVSTLRDEGVGKKSLEGNVTEEA
GHLCDTFAKEAEHPFNPSILLSKAVSNVIASLVYARRFEYEDPFRNMLKTLKSSFGE
DTGFMAEVLNAIFILLOIPGLPGKVFPKLNSFIALVOKMLIEHKKSWDPAQPRDMTD
AFLAEMOKAKGNPESSFNDENLRLVVIDLFMAVGHTSTTLSWALLLMILHDDVGRRV
HEEIDEVIGQVLRPEMADQARNDLTNAVIHEVQRFADIVPTNIPHMTSRDIKFQGFLI
PKGTTLIPNLSSVLEDETVWEKFLRFHPEHFLDAGGNEVKHEAFMPFSAGRRACLGEP
                                                                                                                                                                                                                                       LARMELFLFFTCLLQRFSFSVLAGRPRPSTHGVYALPVTPQPYQLCAVAR® 466 c 437 g 374 t
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/db_xref="taxon:10116"
<1. .1624
                                                                                                                                                                                                                                                                                                                                                                                                                        /product="CYP450 mRNA" 51. .1553
                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA41055.1"
/db_xref="GI:203836"
                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                          /note="debrisoquine 4-hydroxylase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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95.28;
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 male) liver,
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Pred. No. 54;
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Rattus norvegicus
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561 GCGTGGGCAAGAATCGCTGG 581
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                                                                                   2 (bases 1 to 2763)
Wright,R.J., Stephens,C., Zweiger,G., Shapiro,L. and Alley,M.R.K.
Direct Submission
                                                                                                                                                                                                                                       1 (bases 1 to 2763)
Wright, R., Stephens, C., 2
Caulobacter Lon protease
                                                                                                                                                                                                                                                                                                            Caulobacter crescentus
Caulobacter crescentus
Bacteria; Proteobacteria; alpha subdivision;
                                       Submitted (24-APR-1996) Developmental Biology, Stanford Beckman Center B300, Stanford Medical Center, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter crescentus U56652
                                                                                                                                                                                                Genes Dev. 10 (12),
                                                                                                                                                                                                                       of DNA methylation
                                                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
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Four species of cDNAs for cytochrome P450 isozymes immunorelated to P450C-M/F encode for members of P450IID subfamily, increasing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P45UC-M/F encouse to manager of members within the subfamily number of members within the subfamily 156 (2), 681-688 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1698)
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Location/Qualifiers
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HEEIDEVIGQVRRPEMADQARMPFTNAVIHEVQRFADIVPTNIPHMTSRDIKFQGFLI
PKGTTLIPNLSSVLKDETVWEKPLRFHPEHFLDAQGNEVKHEAFMPFSAGRRACLGEP
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DRPLLFIYNHLGYGDKSKGVVLAPYGEBWREORRFSVSTLRDEFUGKKSLEQWYTEEA
GHLCDTFAKEAEHPPNPSILLSKAVSNVIASLFVARRFEYEDDFFNNHLKTLKESFGE
DTGFMAEVLNAIPILLQIPGLPGKVFPKLNSFIALVDKMLIEHKKSMDPAQPPRDMTD
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/db_xref="GI:203824"
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125. .1627
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/db_xref="taxon:10116"
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95.2%;
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Pred. No. 54;
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has a critical role i
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                                                                                                                                                                                                                                                                                                                                   Caulobacter
                                         Stanford University
Stanford, CA
                                                                                                                                                                                                                                                              and Alley, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligo capping; fis (full insert sequence). Homo sapiens fetal brain cDNA to mRNA, clone_lib:OCBBF2 clone:OCBBF2011067.
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan C. Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan C. Research connics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK096600 2827 bp Homo sapiens cDNA FLJ39281 fis, to Homo sapiens cingulin mRNA.
                                                                                                                                                             Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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MSPMSAESTVYRNYLDWLLSIPWGKAKTKKIDLYESERY
AVQARTNSLKOPILCLLOPPOYGKTSLGKSIAKATGREFVRAHSLGGVERVKERIEYL
AVQARTNSLKOPILCLLOPPOYGKTSLGKSIAKATGREFVRAHSLGGVERVKERIEYRI
TYIGSMFGKVVOSMKKAKTTNAFVLLDEIDKMGSDYRGDPASALLEVLDPSQNSTFGD
HYLEVSMKKAKTTNAFVLLDREIDKMGSDYRGDPASALLEVLDPSQNSTFGD
HYLEVSTPDKAIRDLIRYYTRAGVELDRMEIIR 1F0TBELEIAKRHILFKLAK
DHGLKPAEFIYPDKAIRDLIRYYTREAOVRSLERELGAKRHVRDLARRHILFKLAK
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ESYYEAQIGEVSEDDGAGPEAEGLSRAVVEQFENYVKLNKKVPPEALASIPQIAEPGK
LADSIRAHLSVKIGDKQNLLEIFDVVKRLEKVFALMEGEISVLQVEKKIRSRVKRQME
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MVSVLTGIPIRKDIAMTGEITLRGRVTAIGGLKEKLLAALRSGVKTVLIPQENEKDLA
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/db_xref="GI:1667399"
/translation="MSELRTLPVLPLRDIVVFPHMVVPLFVGRDKSVRALEEVMRGDK
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             Strausberg,R
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                          Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/note="Incyte ID No: LI:332161.1:2000SEP08"
840 c 927 g 688 t
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/note="cloning vector: pME18SFL3"
750 c 983 g 406 t
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/clone_lib="OCBBF2"
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I (bases 1 to 6710)

I (bases 1 to 6710)

Fuchs, T., Wiget, P., Osteras, M. and Jenal, U.

Frecise amounts of a novel member of a phosphotransferase superfamily are essential for growth and normal morphology Caulobacter crescentus

Caulobacter crescentus

Mol. Microbiol. 39 (3), 679-692 (2001)
                                                                                                                                                                                                                                         AJ010321.1 GI:3688203 cicA gene; clpP gene; ClpX gene; gene; trigger factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shohiyuki and Plero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Anup Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                               Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                  Caulobacter crescentus
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                       Caulobacter.
                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Caulobacter
                                                                                                                                                                                                                                                                                                                                  genes
                                                                                                                                                                                                                                                                                                                                                                          CAJ10321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prediction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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996 c 1016 g 729 t
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LIVQIKGSVEDIPVMLVGNKCDETQREVDTREAQAVAQEWKCAFMETSAKMNYNVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="similar to Rig protein"
/protein_id="AAH30660.1"
/db_xref="GI:21040535"
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/clone_lib="NIH_MGC_95"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jenal, U
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1086. .1
                                                                                                          /translation="MAKGLSASRPMTGEMGHEPLLVAFDFDGTLTVKDSFNAFLKWRA
GPRWSFGVLRLTPALIAYVFDRNRGKLKAAAVRQFLKGATVAQIENDARAFAEAFAPS
LLRPDAVAVWRGWRAKGAKMVIVTASPDLIVAPFARGLGADLLIGTRLRCSDDGRILG
                                                                                                                                                                                                                                                                                                                                               /evidence=experimental complement(1894..2544) /gene="cicA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mmydpvstammlvpmvveQtsrgerafdifsrllkeriifltgp
vedgmaslicaQllflesenpkkeiamyinspggvvtaglaiydtmQyikspvstvcm
gmaasmgslllaagaagQrislpnarimvhQpsggfrgQasdierhaediiktkrrln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SWISS-PROT:087705"
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/protein_id="CAA09091.1"
/db_xref="GI:3688206"
/db_xref="SWISS-PROT:087707"
                                                                                                                                                                                                                                                                                                                              complement(1894. .2544)
                                                                                                                                                                                                                                                                                                                                                                                                              /gene="cicA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="endopeptidase clp"
/protein_id="CAA09090.1"
/db_xref="GI:3688205"
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DAEKTEDQLKDEYKKIAERRVRLGLVLAEIGRKNDVVVTDQELTDAIMREARQYGAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="trigger factor
/protein_id="CAA09089.1"
/db_xref="GI:3688204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Caulobacter cro/
/strain="NA1000 syn-1000"
                                                                  2664. .4218
                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SWISS-PROT:087706"
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1183. .1815
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/note="cicA"
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/transl_table=11
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SOURCE
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Rattus norvegi
X52027 X52455
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2107330
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The rat P450 IID subfamily: complete sequences of four closely linked genes and evidence that gene conversions maintained sequence homogeneity at the heme-binding region of the cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytochrome; Cytochrome P450; cytochrome Rattus norvegicus.
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/gene="clpx"
a 2061 c 2
            /gene="P450 IID2"
519. .>4634
                                                                                   /clone_
                                                 /note="putative and atypical" 519...4634
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ERRTGEILRNVEPDDLQRFGLIPEFIGRLPVVATLEDLDEAALVKILTEPKNAFVKQY
QRLFEMENIGLTFTEDALHQVAKKAIARKTGARGLRSIMEGILLETMFELPTYEGVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mtkaasgdtkstlycsfcgksqhevrkliagptvpicdecvelc
MDIIREBHKIAFVKSKDGVPTPREICEVLDDYVIGGGHAKVLAVAVHHYKRLNHAS
KNNDVELAKSULLVGPTGCKTLAQTLARIDVPFTMADATTLTEAGVGEDVDU
VLKLLQAADYNVERAQRGIVYIDEIDKISRKSDNPSITRDVSGEGVQQALLKIMEGTV
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/db_xref="GI:3688207"
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/transl_table=11
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2758. .2793
/gene="P450 IID2"
                                                                                                                    /tissue_
                                                                                                                                   /clone="lambda rG10"
                                                                                                                                                  /db_xref="taxon:10116"
                                                                                                                                                                  /strain="Sprague-Dawley
                                                                                                                                                                                  /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
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                                                                                                   lib="lambda EMBL3"
                                                                                                                    type="liver"
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Pred. No. 57;
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LARMELFLFTFCLLQRRSFSVLAGRPRPSTHGYYALPVTPQPYQLCAVAR*
Join(592...780,1394...1565,1799...1951,2025...2185,2861...)
3216...3357,3545...3732,4063...4204,4305...4480)
/gene="P450 IID2"
                               4063.
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DRPLLPIYNHLGYGNKSKGVVLAPYGPEWREQRRFSVSTLRDFGVGKKSLEQWVTEEA
GHLCDTFAKEAEHPFNPSILLSKAVSNVIASLVYARRFEYEDPFFNRMLKTLKESFGE
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3216. .3357,3545. .3732,4063. .4204,4305. .4483)
/gene="P450 IID2"
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/gene="P450 IID2"
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AFLAEMQKAKGNPESSFNDENLRLVVIDLFMAGMVTTSTTLSWALLLMILHPDVQRRV
HEEIDEVIGQVRRPEMADQARMPFTNAVIHEVQRFADIVPTNIPHMTSRDIKFQGFLI
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/protein_id="CAA56269.1"
/db_xref="G1:57812"
/db_xref="SWISS-PROT:P10634"
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2861. .3037,3216. .3357,3545. .3732,4063. .4204,4305.
/gence-"P450 IID2"
/evidence-experimental
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/gene="P450
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/gene="P450 IID2"
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              1063. .4204
/gene="P450
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KEYWORDS
SOURCE
ORGANISM
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VERSION
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MEDLINE
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Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Laub, M.T., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
                                                                                                                                                                              Submitted (31-JAN-2001) The I
Medical Center Dr. Rockville,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haft,D.H., Kolonay,J.F., Smit,J., Craven,M.B., Khouri,H., Shetty,J., Berry,K., Utterback,T., Tran,K., Wolf,A., Vama Ermolaeva,M., White,O., Salzberg,S.L., Venter,J.C., Shapi
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Eisen, J., Heidelberg, J.F., Alley, M.R., Ohta, N., Maddock, J.R.,
Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D.,
Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, N.L.,
                                                                                                                                                                                                                                                                                                                                                                                                            Complete genome sequence of Caulobacter crescentus Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
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Caulobacter crescentus CB15
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Caulobacter crescentus
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                                                                       /gene="
131. .2
                        /gene="tRNA-Asp-1"
/product="tRNA-Asp"
272. .348
                                                                                                    /db_xref="taxon:190650"
131. .207
                                                                                                                                  /organism="Caulobacter crescentus CB15"
/strain="CB15"
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1783 c 2019
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/translation="MSELRTLPVLPLRDIVVFPHMVVPLFVGRDKSVRALEEVMRGDK
QILLVTQKNSADDDPAPGDIFEVGVLATVLQLLKLPDGTVKVLVEGKARAAVVSFTDQ
ESYYEAQIGEVSEDDGAGPEAEALSRAVVEQFENYVKLNKKVPPEALASIPQIAEPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="DNA-binding protein HU"
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complement/^^^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLSPKDRLLVFAGRPAREKKLDVLVAAVERLGDPYKLLFVGAGGGAPVSDRTLCIDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3109. .3387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSSASAHAGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLGFHRYWLAEHHNMPGIASAATAVVIGQIAAATTTIRVGSGGVMLPNHAPLMVAEQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1417. .2625)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GELAGLDHTLQYAAIGSPETVRRKIDRVLELTGADELMAAAQIHDHAARRRSYEILAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                              .5930)
                                                                                                                                                                                                                                                                                                                 by match
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                                                                                                                                                                                                    LA.
                                                                                                                                                                                                                                                                                                              protein
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DVPQTVKDGLEIIPVSTVDEVLKHALTGPLTPVEWNEAEEPITTSAKKDDGDSDAMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKDVMKESIAAANSYVRSRALQFGIKPPVFEKTDVHIHVPDGATPKDGPSAGIAMALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHGLKPAEFIVPDKAIRDLIRYYTREAGVRSLERELGALARKTVRDLAREKVASITID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="CC1961"
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                                                                                                                                                                                                                                                                                                                                                    to TIGR protein family HMM
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CDS

gene

CDS gene

GKSLKAKDGDQLLIDFVGTIDGVEFAGGKAEGAELVLGSGQFIPGFEDQLVGAKPGDD

gene

CDS

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GG
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BASE COUNT 1854 a 3619 c 3396 g 2091 t

Best Local Matches 2 Query Match 20; Similarity Conservative 92.4%; 95.2%; 0; Score 19.4; Pred. No. 57; Mismatches DΒ 1; 1; Length 10960; Indels 0; Gaps

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CDS

gene

Search completed: March Job time: 77.4223 secs 23, 2003, 16:10:00 밁 Ş

1 GCGTGGGCAAGAACTCGCTGG GCGTGGGCAAGACCTCGCTGG 4847

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Perfect score:
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                                                                                                                                                                                                                                                                                                                           d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
19.4
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Gapop 10.0 , Gapext 1.0
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Listing
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
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702
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               ABQ72525
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1936.775 Million cell updates/sec
                                                                                                                                                                                                                   Description
                                      Cytochrome P450IId
Drosophila melanog
Gene #3691 used to
                                                                                                      Human MDDT encodin
Partial human cyto
DNA sequence of am
                                                                                                                                                                            Human MDDT
                                                                                                                                                                            encodin
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molecule polynucleotide; cancer; AIDS; allergy; multiple sclero	ID NO 77. on and treatment titis; psoriasis atory disorder;	entry) DNA SEQ I detection er; hepati inflammat	ത്ര ത	1.0 0	25; -200 MDDT MDDD MDD erat mune	ABQ72525 03-SEP-2 Human MD Human; M prolifer autoimmu
	ALIGNMENTS	124	; cDNA;	tandard;	25 s	SULT 1 Q72525 ABQ725
	AT TONMENTS					
Human	2	24	σ.	80.0		45
Drosophila	ABL11392	23	3188	00		44
Ge	ABN95766	24	2336	0		42
Oncogene R	AAT08552	17	2336	0.		41
Human	ABL50225	24	2223	0 9		40
Human	ABL50193	24	2223	0:		ω u
	ABQ90836	24	1629	0		37
Drosophila melanog	ABL11393	23	1188	0		36
DNA	AAS82965	23	1078	0		35
Mouse	ABI 19215	24	1021	0:		ω υ 4- υ
DNA	AAS82963	2 2	421	0		່ວນ
Drosophila melanog	ABL15252	23	14112	2		ω
Drosophila	ABL04/44	23	4389	N.		30
Drosophila melanog	ABL15253	2 2 3 3 3	1471	82.9	17.4	2 8
Dro	ABL04759	23	922	2		27
Hun	AAD34213	24	9432	4		26
Hun	ABO72364	24	6472	٠.		2,4
Drosophila me	ABL11094	2 2	3493	4.		2 23
Drosophila melanog	ABL14158	23	2951			22
Hur	AAD09937	22	1593			21
Debrisoquine hydro	AAQ12893	12	1586	4		20
Cytochrome P450IId	AAV19496	19	1545	•		19
Human	AB072216	24	1494	٠.		18
Human	AAT17388	17	1494	٠.		17
Human	AAT2839/	17	1494	٠.		1 5
Human	AAT28396	17	1494	٠. ۵		14
Human	2839	17	9	٠.	•	13
Human	8773	16	9	84.8		12
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06-SEP-2000; 2000US-230505P.
06-SEP-2000; 2000US-230514P.
06-SEP-2000; 2000US-230515P.
06-SEP-2000; 2000US-230517P.
06-SEP-2000; 2000US-230518P.
06-SEP-2000; 2000US-230519P. autolimnune disorder; inilammatory disorder; aliergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout; neuroprotective; antirheumatic; antiarthritic; gene; ss. 06-SEP-2001; 2001WO-US27628 23-MAY-2002 WO200240715-A2 sapiens

Gene #3691 us Human CYP2D6

gene

Human auxillary

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                                                                                                                                        CC treatment (MDDT) polypeptide (I) selected from a polypeptide having a CC sequence selected from 254 sequences (ABBP51231-ABP51484) given in the CC sequence selected from 254 sequences (ABBP51231-ABP51484) given in the CC sequence selected from 254 sequences (ABBP51231-ABP51484) given in the CC sequence selected from 254 sequences (ABBP51231-ABP51484) given in the CC sequence state of (I). (I) is useful for screening a compound for CC immunogenic fragment of (I). (I) is useful for screening a compound that CC specifically binds (I) or modulates the activity of (I), and for CC screening a compound for effectiveness in altering expression of a target CC polynucleotide comprising. Oligonucleotides and antibody by hybridoma technology. CC Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for CC detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the CC expression of MDDT in a bindogical sample, for detecting (I) in a sample, caspociated with decreased or increased expression of functional MDDT. CC associated with decreased or increased expression of functional MDDT. CC associated with aberrant expression of MDDT. The manual of the model haver the disorders are selected from a cell proliferative disorder such as arteriosclerosis, callergy, anamala, asthma, atherosclerosis, gout, multiple sclerosis or condition companies and cancer and an antible schemals, asthma, atherosclerosis, sout, multiple sclerosis or condition componies or transgenic animals to model human diseases, in sommatic or componies conductions of a targenic animals to model human diseases, in sommatic or componies or conditions of a targenic animals to model human diseases, in sommatic or condition or conditions of a targenic animals to model human diseases.
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06-SEP-2000;
06-SEP-2000;
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06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
07-SEP-2000;
07-SEP-2000;
                                                                                                                                                                                                       germline gene therapy, to generate a transcript image of a tissue or cel
type, for detecting differences in the chromosomal location due to
translocation or inversion among normal, carrier or affected individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones AL, Yu
Momiyama MG,
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 350-351;
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)B; ABP51307.
GCGTGGGCAAGAGCTCGCTGG
                                                                                                                                                                                          hybridisation
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                                                                  Similarity 95.:
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INCYTE GENOMICS INC
                                                                                                                                        1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n disease detection and treatment polypeptide, useful in prevention or treatment of cell proliferative disorders e.g erosis, cirrhosis and an autoimmune/inflammatory disorder
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G, Bradley
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                                                                                                                                        B₽;
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lley DL, Rohatgi SD, Harris B,
lta CH, David MH, Panzer SR, F
NJ, Chang SC, Au AP, Inman RR;
                                                                                                                                    230 A; 436 C;
                                                                                    92.4%;
95.2%;
                                                                                                                                                                                       probes
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                                                                                  . 28;
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                                21
                                                                  0;
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                                                                                  Pred.
                                                                                                    Score 19.4;
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                                                                    Mismatches
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                                                                                                                                    T; 0
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B, Roseberry
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IF, Yap PE,
                                                                                                                                      other;
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                                                                  0;
                                                                                                                                                                                       genomic
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Dahl CR;
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RESULT 2
ABQ772648
ID ABQ772648
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AC ABQ7
XX A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2001;
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2000US-23059SP.
2000US-23059RP.
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2000US-230610P.
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Gerstin Marwaha s, EH, MG, Yu Lincoln SE, Altu Yu JY, Wright RJ, G, Bradley DL, Ro Chen AJ, Peralta CH, Chang Altus Altus CM, Dufour GE, Chalup MS, H RJ, Gietzen D, Liu TF, Yap PE, Rohatgi SD, Harris B, Roseberry David MH, Panzer SR, Flores V, D ang SC, Au AP, Inman RR; Dahl

WPI; 2002-527544/56. P-PSDB; ABP51431.

Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.

Claim Page 414; 618pp; English.

immunogenic fragment of (I). (I) is useful for screening a compound fo effectiveness as an agonist or antagonist, for screening a compound th specifically binds (I) or modulates the activity of (I), and for preparing a polyclonal or monoclonal antibody by hybridoma technology. Nucleic acids (II) (ABQ72449 ABQ72700) encoding (I) are useful for screening a compound for effectiveness in altering expression of a tar treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51231-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or The invention relates to an isolated human disease detection target for

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RESULT
ABK8722
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CC in a diagnostic test for a condition or a disease associated with the 
CC expression of MDDT in a biological sample, for detecting (I) in a sample, 
CC and for purifying (I) from a sample. A composition comprising (I), an 
CC agonist or antagonist is useful for treating a disease or condition 
CC associated with decreased or increased expression of functional MDDT.

CC (I) or (II) are useful for diagnosing, treating or preventing disorders 
CC associated with aberrant expression of MDDT, where the disorders are 
CC selected from a cell proliferative disorder such as arteriosclerosis, 
CC cirrhosis, hepatitis, psoriasis, and cancer and an 
CC autoimmune/inflammatory disorder such as AIDS, Addison's disease, 
CC allergy, anaemia, asthma, attherosclerosis, gout, multiple sclerosis or 
CC armelian for transgenic animals to model human diseases, in somatic or 
CC armelian for transgenic animals to model human field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                02-OCT-2000;
10-NOV-2000;
10-NOV-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                           tumour diagnosis; disease predisposition; forensic; paternity; crop cultivation; animal breeding; expression profiling; infectious organism; plant; food safety; cytochrome 2D6;
                                                                                                                                                                                                                                                                                                                                                                                                                                         human genetic disease; pathogenic microorganism; bladder carcinoma; sickle-cell anaemia; thalassaemia; Alzheimer's disease; phenylketonuria; galactosaemia; Wilson's disease; diabetes insipidus; neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              germline gene therapy, to generate a transcript image of a tissue or cel type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic
                  10-NOV-2000;
                                                                                                                                 01-OCT-2001;
                                                                                                                                                                13-JUN-2002
                                                                                                                                                                                                WO200246447-A2
                                                                                                                                                                                                                                                                               variation
                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3061 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                            familial hypercholesterolaemia; genetic analysis; hereditary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Restriction endonuclease recognition sequence; RERS; drug resistance;
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2000US - 237409P.
2000US - 247166P.
2000US - 247167P.
2000US - 247172P.
2000US - 247173P.
2000US - 247275P.
2001US - 263971P.
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                                                                                                                                 2001WO-US30742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytochrome 2D6 gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising.
                                                                                                                                                                                                                                                              replace
/*tag=
                                                                                                                                                                                                                                               /standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 A;
                                                                                                                                                                                                                                                                                                                                                            polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                               (65..67,GG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotides and antibodies are or for assessing toxicity of a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                 SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                            gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell
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CC method of the invention utilises a pair of oligonucleotide primers
CC comprising a nucleotide sequence that is complementary to a nucleotide
CC sequence of the target nucleic acid or complementary to a nucleotide
CC sequence of the complement of the target nucleic acid and further
CC comprising part of an interrupted restriction endonuclease recognition
CC sequence (RERS). The invention is useful for identifying a nucleotide at
CC a defined position in a single-stranded target nucleic acid. The defined
CC position may be polymorphic or associated with a disease, especially a
CC human genetic disease, or drug resistance of a pathogenic microorganism.
CC The defined position is associated with a disease, including a human
CC genetic disease e.g. bladder carcinoma, sickle-cell anaemia, or
CC wilson's disease, diabetes insipidus, familial hypercholesterolaemia, or
CC wilson's disease, diabetes insipidus, familial hypercholesterolaemia, or
CC for hereditary disease, tumour diagnosis, disease predisposition,
CC for hereditary disease, including a human and/or cell function and/or disease marker genes, and
CC cause infectious disease in plants or animals and/or that are related to food safety. The method is useful for determining gene variations in
CC are involved in the recognition of variable, antigen-specific regions that
CC are involved in the recognition of variable antigen-specific regions that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2001;
21-JUN-2001;
27-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying single nucleotide polymorphisms at defined positions in target nucleic acids, by utilising oligonucleotide primers that contain a part of an interrupted restriction endonuclease recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new method of identifying a nucleotide at a defined position in a single stranded target nucleic acid. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van
                                                nucleic acid sequence represents the partial human cytochrome sequence that was used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J,
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2001US-300319P.
2001US-300350P.
2001US-301394P.
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A; 40
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Best Loc
Matches
                                   Query Match
Local
                       l Similarity
19; Conser
                        Conservative
                              84.8%;
90.5%;
           21
                        0;
                                   Score
                              Pred.
                        Mismatches
                            , 17.8; L
                                    DB
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                        Indels
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Sequence

130 BP; 19

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46 G;

25 T; 0 other;

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25-SEP-2002

(first entry)

В Qγ

40

60

Variation site; analysing; point mutation; detecting single nucleotide polymorphisms; paternity dispute; forensic analysis; CYP450.2D6.G1749C; ds. Unidentified DNA sequence of amplifier containing CYP450-2D6-G1749C SNP. detecting prenatal testing; pathogen; SNP;

WO200194546-A2

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RESULT 5
NAV19498
ID AAV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for analysing a variation site in a target polynucleotide. The method comprises contacting the target polynucleotide with multiple copies of a primer hybridising adjacent to, but not including, the variation site in the presence of a mixture of labelled and unlabelled forms of a nucleotide under conditions such that a copy of the primer is extended by incorporation of a labelled nucleotide complementary to a base occupying the variation site in the target polynucleotide; detecting the labelled nucleotide incorporated into the primer as an indication of the variation site base. The methods are useful for analysing variant sites in nucleic acids of interest, including point mutations and single nucleotide polymorphisms (SNP), and for detecting pathogens, paternity disputes, prenatal testing and forensic analysis. This polynucleotide sequence represents the DNA of an amplifier containing the CYP450.2D6.G1749C SNP relating to the
                                                                                                                                   CDS
                                                                                                                                                                                                                                    Cytochrome P450IId6 encoding DNA 349-825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analyzing variant site in target polynucleotide comprises using mixture comprising labeled and unlabeled forms of nucleotide to generate labeled extension products that are characteristic of nucleotide at variant sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2001;
                            24-SEP-1996;
                                                       21-APR-1998
                                                                               JP10101698-A
                                                                                                                                                                       Hepatitis
                                                                                                                                                                                                 autoimmunohepatitis
                                                                                                                                                                                                                                                                                        AAV19498;
                                                                                                                                                                                                                                                                                                                  AAV19498 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                              Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                  165
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                                                                                                                                                                                                                                                                                                                                                                                  GCCTGGGCAAGAAGTCGCTGG
                                                                                                                                                                                              cytochrome P450IId6; liver/kidney microsome; LKM-1; antibody;
munohepatitis type II; AIH type II; hepatitis C virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400
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                                                                                                                                                                         virus
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                          96JP-0273055
                                                                                                                               Location/Qualifiers
1..477
                                                                                                        /product= "cytochrome P450IId6 fragment"
                                                                                                                      /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               84.8%;
90.5%;
                                                                                                                                                                                                                                                                                                                  477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           400;
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ABL14159
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Best Local
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                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventice useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a protein fragment of cytochrome P450IId6 which is recognised by AIH Type IIa/IIb LKM1 antibody. The antigens and their complementing antibodies are used in the detection of auto-immuno-hepatitis type II and hepatitis C.
                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000;
11-JUL-2000;
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P-PSDB; AAW44871.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
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19; Conserv
                                                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M,
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2000US-0614150.
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                                                                                                                                                                                                              36959; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                               PWD,
                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Myers
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                                                                                                                                              invention
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RESULT 7
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Best Local
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Best Local
   Matches
                                                                                                                                                  expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, and the cartest that can be used to monitor disease states.
                                                                                                      drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                The invention relates to a novel method for diagnosing and detecting to progression of liver cancer, hepatocellular carcinoma or metastatic liver cancer from tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of the progression of the carcinoma in a patient.
                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in liver tissue sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                               Sequence 1449
                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 3691; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-426119/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2001; 2001WO-US30589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene #3691 used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCGTGGGCAAGAACTCGCTGG
                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                tissue sample
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 1 Similarity
19; Conserv
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 Conservative
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                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to diagnose liver cancer.
                                                            256 A; 465 C; 439 G;
             84.8%;
90.5%;
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90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peres-Da-Silva
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              Score 17.8; D
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Pred. No. 26;
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   Mismatches
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                                                            289 T;
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                              DΒ
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                                                            0 other;
2;
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                                                                                                                                                                                                                                                                   the level of
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Gaps
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RESULT 9
AAQ87729

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AAQ87729 standard; cDNA; 1494 BP

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RESULT 8
AAD09849
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                                                                                                                                                                                                                                                                                                                                                                                labelled probe to the target sequence amplification product and a second labelled probe to the standard sequence amplification product, second labelled probe to the standard sequence amplification product, detecting the signals from the first and the second probe, and comparing the signals to determine the polymorphism. The method is useful for detecting polymorphism in various nucleic acid sequences e.g. CYF2D6 gene which is a member of cytochrome p430 (CYP) gene family. CYP2D6 plays a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a mutation in target nucleic acid sequence in test sample, amplifying target and standard nucleic acid sequence using primers, hybridizing probes to the products to form hybrids, and detecting
                                                                                                                                                                                                                                                                                      role in the metabolism of several drugs, including those used for treating psychiatric and cardiovascular disorders. Polymorphism in the CYP2D6 gene have varying effect on an individual's ability to metabolise drugs. The method is suitable for detecting amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid sequence using amplification technique. The method involves amplifying the target sequence and a standard nucleic acid sequence using primers to form amplification products, hybridising a first labelled probe to the target sequence amplification product and a
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                           products from multiple and different types of polymorphisms on a single automated platform. The present sequence is human CYP2D6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 30; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for detecting polymorphism in a target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-2000;
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                       GCGTGGGCAAGAACTCGCTGG
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metabolism; psychiatric disorder; cardiovascular disorder; d
GCCTGGGCAAGAAGTCGCTGG
                                                                                            1 Similarity
19; Conser
                                                                                                                                                                                             1450 BP; 270 A; 395 C; 521 G;
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                                                                                              Conservative
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                                                                                                                   84.8%;
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170
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                                                                                                                     Score 17.8;
Pred. No. 29
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                                                                                              Mismatches
                                                                                                                                                                                             264 T; 0 other;
                                                                                                                        29;
                                                                                                                                            DB
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                                                                                                                                          Length
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                                                                                                                                               1450;
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RESULT 10
AAQ87730
ID AAQ87
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AC AAQ87
XX
DT 15-NO
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                                                                                                                                                                                                                                                       The nucleotide sequence of the cDNA coding region for the human CC auxillary cytochrome P450 species 266. The gene encodes a protein of 497 CC amino acids. The cDNA was amplified by PCR using the primers AAQ87763-6. CC The product was cloned into the yeast expression vectors PAHSN or PAHRR CC to produce the vectors P2D6 for the expression of the cytochrome P450 celuctase. CC The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced CC human cytochrome P450 molecular species 1A2 (AAQ87714), 2C9 (AAQ87715), or 3A4 (AAQ87717) or their auxillary species and CC variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused CC rotein or in cell extracts, and analysing the resulting metabolite to determining whether the chemical compound. The method is useful for CC converted into a carcinogenic or mutagenic form through metabolism in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                           Query Match
              15-NOV-1995
                                                                AAQ87730 standard;
                                        AAQ87730;
                                                                                                                                                                                                                                                       Sequence 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase {
m expression}
                                                                                                                                          428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR72375
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Yabusaki Y;
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(SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-1993;
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20-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytochrome P450; amplification; PCR; yeast NADPH-P450 reductase; safety; fusion carcinogen; mutagen; liver metabolism; ds.
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                                                                                                                                       GCCTGGGCAAGAAGTCGCTGG 448
                                                                                                                                                                 GCGTGGGCAAGAACTCGCTGG 21
                                                                                                                                                                                                l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko H,
                                                                                                                                                                                                Conservative
          (first entry)
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                                                                                                                                                                                                                                                       В₽;
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93JP-0201120.
93JP-0208279.
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                                                                                                                                                                                                                                                   248 A; 508 C; 446 G;
                                                                 CDNA; 1494
                                                                                                                                                                                                          84.8%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komai
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                                                                                                                                                                                                           Score 17.8;
Pred. No. 29;
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                                                                  ВP
                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion protein; metabolite; m; ds.
                                                                                                                                                                                                                                                 292 T; 0 other;
                                                                                                                                                                                                                        DB 16;
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                                                                                                                                                                                                                       Length 1494;
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RESULT 11
AAQ87731
                                                                                                                                                                                                                                                                                                                                                          CC cloned into the yeast expression vectors pAAH5N or pAHRR to product was correctors p2D6 variant 1 for the expression of the cytochrome P450 alone CC or p2D6R variant 1 for co-expression of the cytochrome P450 alone CC reductase. The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly CC produced human cytochrome P450 molecular species 1A2 (AAQ87714), 2C9 CC (AAQ87715), 2E1 (AAQ87716-32), and yeast NADPH-P450 or their auxillary species and variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a CC fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for CC determining whether the chemical compound. The method is useful for CC converted into a carcinogenic or mutagenic form through metabolism in the CC liver.
                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                               Query Match
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20-JUL-1993;
30-JUL-1993;
AAQ87731 standard; cDNA; 1494
                                                                                                                                                                                                                                                                                                                         Sequence 1494 BP; 248 A; 509 C; 446 G; 291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The nucleotide sequence of the cDNA coding region for the human auxiliary cytochrome P450 species 2D6 variant 1. The gene contains a change at base 886 from T to C as compared to the wild type sequence (AAQ87729). This changes the amino acid residue 296 from Cys to Arg. cDNA was amplified by PCR using the primers AAQ87763-6. The product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
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P-PSDB; AAR72376.
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Yabusaki Y;
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(SUMO ) SUMITOMO CHEM CO LTD
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les 19; Conserv
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                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93JP-0180246.
93JP-0201120.
93JP-0208279.
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                                                                                                                                                                                                                                                84.8%;
90.5%;
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                                                                                                                                                                                                                                                   Score 17.8;
Pred. No. 29;
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AAQ87731;

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428

GCCTGGGCAAGAAGTCGCTGG

448

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                                                                                    CC auxiliary cytochrome P450 species 2D6 variant 2. The gene contains at bases 886: T to C and 1457: C to G as compared to the wild type sequence (AAQ87729). These change the amino acid residues 296: Cys C to Arg and 486: Thr to Ser. The cDNA was amplified by PCR using the C primers AAQ87763-6. The product was cloned into the yeast expression CC vectors pAADS or pAHRRR to produce the vectors p2D6 variant 2 for the C expression of the cytochrome P450 alone or p2D6R variant 2 for the C co-expression with the yeast NADPH-P450 reductase.

CC The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced thuman cytochrome P450 molecular species 1A2 (AAQ87714), 2C9 (AAQ87715), C2E1 (AAQ87716), or 3A4 (AAQ87717) or their auxillary species and CC variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused CC variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused CC converted into a carcinogenic or mutagenic form through metabolite to cassess the safety of the chemical compound, or its metabolite, will be CC converted into a carcinogenic or mutagenic form through metabolism in the
                                              Query Match
Best Local
                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1993;
20-JUL-1993;
30-JUL-1993;
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variation
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                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                             Examples; Page 91-93; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                   Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
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            Н
                                                                                                                                                                                                                                                                                                                                                                                                                          1995-116991/16
DB; AAR72377.
           GCGTGGGCAAGAACTCGCTGG
auxillary cytochrome
                                    . Similarity
19; Conserv
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SUMITOMO CHEM CO LTD.
                                                                                    1494
                                    Conservative
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93JP-0201120.
93JP-0208279.
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                                                                                    248 A;
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                                               84.8%;
90.5%;
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acid
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acid
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from Cys
                                                          Score 17.8;
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                                               Pred.
                                  Mismatches
                                                                                  447 G;
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Arg"
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                                                          Length 1494;
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Query Match
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Matches 19; Conser

Conservative

0; Pred. No. Score 17.8; C; 447 G;

Mismatches

29;

DΒ

16; 2,

Length Indels

1494; 0;

Gaps

0,

84.8%; 90.5%;

Sequence

1494

BP;

248 A; 507

292 T; 0 other;

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RESULT 12
AAQ87732
The nucleotide sequence of the cDNA coding region for the human compound at lary cytochrome P450 species 2D6 variant 3. The gene contains a CC change at base 1457 from C to G as compared to the wild type sequence CC (AAQ87729). This changes the amino acid residue 296 from Thr to Ser. The CC change amplified by PCR using the primers AAQ87763-6. The product was compound into the yeast expression vectors pAAH5N or pAHRR to produce the cytochrome P450 alone CC or p2D66 variant 3 for the expression of the cytochrome P450 alone CC reductase. The vectors are used in a method for evaluating the safety of CC reductase. The vectors are used in a method for evaluating the safety of CC produced human cytochrome P450 molecular species 1A2 (AAQ87714), 2C9 CC (AAQ87715), 2E1 (AAQ87716), or 3A4 (AAQ87717) or their auxillary species and variants (AAQ87718), and yeast NADPH-P450 reductase, either as a CC fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or its metabolite, will be converted into a carcinogenic or mutagenic form through metabolism in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1993;
20-JUL-1993;
30-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Examples; Page 95-97; 124pp; English.
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P-PSDB; AAR72378.
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Yabusaki Y;
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(SUMO ) SUMITOMO C
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1457
/*tag= a
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a yeast NADPH-P450 reductase
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RESULT 13
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                                                                                                                   CC This is the nucleotide sequence of the human cytochrome P450 molecular CC species 2D6 variant #1 which encodes a protein of 497 amino acids. The CC gene was amplified from a human liver derived cDNA library as 2 CC fragments of 0.4 and 0.9 kb using primers AMT26933-6. The prod. was Cloned into the yeast expression vector pAAH5N to generate plasmid p2D6 CC for prodn. of the cytochrome only or into the vector pAHRR to generate CC the plasmid p2C6R for co-prodn. with the yeast NADPH-P450 reductase. The sequence is placed under control of the yeast ADH gene promoter and CC terminator. The vectors are used in a method for evaluating the safety of CC a cpd. by reacting the test cpd. with recombinantly produced human CC tytochrome P450 mol. species 1A2 (AAT28380), 2C9 (AAT28381), 2E1 CC (AAT28382), 3A4 (AAT28383) or their variants (AAT28384-98) together with cyest NADPH-P450 reductase (either as a fused protein or as a cell extract) and analysing the resultant metabolite. The cpd. is considered considered if it is detoxified or not rendered carcinogenic cpd. Sequence 1494 BP; 248 A; 508 C; 446 G; 292 T; 0 other;
                                                               Matches
                                                                              Query Match
Best Local
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20-JUL-1993;
30-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 49-51; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen
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                GCGTGGGCAAGAACTCGCTGG
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DB; AAR93182.
GCCTGGGCAAGAAGTCGCTGG 448
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                                                                              Similarity
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94JP-0136053.
93JP-0201120.
93JP-0208279.
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                                                                            84.8%;
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Pred.
                                                               Mismatches
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                                                                                        Length
                                                            Indels
                                                                                           1494;
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RESULT 14 AAT28396

Human cytochrome P450 molecular species

2D6 variant #3

0;

11-OCT-1996

(first entry)

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RESULT 15
AAT28397
XEXTXCX
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                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of the human cytochrome P450 molecular CC species 2D6 variant #2 which encodes a protein of 497 amino acids. The CC gene was amplified from a human liver derived CDNA library as 2 CC fragments of 0.4 and 0.9 kb using primers AAT26953-6. The prod. was CC cloned into the yeast expression vector PAAH5N to generate plasmid p2D6 CC for prodn. of the cytochrome only or into the vector pAHFN to generate CC sequence is placed under control of the yeast NADPH-P450 reductase. The CC sequence is placed under control of the yeast NADPH-P450 reductase. The CC cytochrome P450 mol. species 1A2 (AAT28380), 2C9 (AAT28381), 2E1 CC (AAT28382), 3A4 (AAT28383) or their variants (AAT28384-98) together with yeast NADPH-P450 reductase (either as a fused protein or as a cell cyeast NADPH-P450 reductase (either as a fused protein or as a cell cyeast NADPH-P450 reductase (either as a fused protein or as a cell cartact) and analysing the resultant metabolite. The cpd. is considered "safe" if it is detoxified or not rendered carcinogenic or "unsafe" if it is not detoxified or is metabolised to a carcinogenic cpd. Sequence 1494 BP; 248 A; 509 C; 446 G; 291 T; 0 other;
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                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel method for the evaluation of the safety of a human cytochrome P450 and yeast NADPH reductase to the analyte cpd. is detoxified or metabolised to a
                                                                                                          AAT28397 standard;
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20-JUL-1993;
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                                                                                                                                                                                          428
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                                                                                                                                                                                                                                                                    Local
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19; Conser
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93JP-0201120.
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                                                                                                          DNA; 1494
                                                                                                                                                                                                                                                                 84.8%;
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                                                                                                                                                                                                                                                     Score 17.8; D
Pred. No. 29;
0; Mismatches
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determine whether
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH gene promoter;
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CC species 2D6 variant #3 which encodes a protein of 497 amino acids. The cgene was amplified from a human liver derived cDNA library as 2 CC fragments of 0.4 and 0.9 kb using primers AAT26953-6. The prod. was CC cloned into the yeast expression vector pAAH5N to generate plasmid p2D6 CC for prodn. of the cytochrome only or into the vector pAHFR to generate CC the plasmid p2C6R for co-prodn. with the yeast NADPH-P450 reductase. The CC sequence is placed under control of the yeast NADPH-P450 reductase. The CC expl. by reacting the test cpd. with recombinantly produced human CC cytochrome P450 mol. species 1A2 (AAT28380), 2C9 (AAT28381), 2E1 CC (AAT28382), 3A4 (AAT283838) or their variants (AAT28384-98) together with cc yeast NADPH-P450 reductase (either as a fused protein or as a cell cextract) and analysing the resultant metabolite. The cpd. is considered crimer if it is detoxified or not rendered carcinogenic or "unsafe" if it is detoxified or rot rendered carcinogenic cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1994;
20-JUL-1993;
30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-182311/19.
P-PSDB; AAR93184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer; liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter; evaluation; safety; fusion protein; metabolite; detoxification; carcinogenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 53-55; 74pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0136053.
93JP-0201120.
93JP-0208279.
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               84.8%;
90.5%;
                    Pred. No.
                                    Score 17.8;
                  29;
                                    DB 17;
                                  Length 1494;
0;
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Search completed: March 23, 2003, 15:20:21 Job time: 26.9179 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
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21
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Match Length DB
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      Published_Applications_NA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                    : /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                         1449
    0 US-09-960-352-10636

0 US-09-960-352-2434

0 US-09-960-352-10478

US-09-960-352-13143

10 US-09-983-965-4246

10 US-09-983-965-4253

10 US-09-960-352-4253

10 US-09-960-352-5830

10 US-09-960-352-5830

10 US-09-764-864-354

10 US-09-764-864-354

10 US-09-764-864-354

10 US-09-960-312-1367

10 US-09-978-650-11

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US-10-108-605-44
US-10-014-717-1
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US-09-747-538-1
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_NEW_PUB.seq:*
Sequence 3688, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 10636, A
Sequence 10478, A
Sequence 13143, A
Sequence 4246, Ap
Sequence 4253, Ap
Sequence 453, Ap
Sequence 354, App
Sequence 354, App
Sequence 354, App
Sequence 367, App
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 1463, Ap
Sequence 1463, Ap
                                                                                                                                                                                                                                                                                                     Description
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ALIGNMENTS

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RESULT 2
US-09-747-538-1
; Sequence 1, Application US/09747538
; Patent No. US20020102549A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 x07618 US-09-880-107-3688
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                                                                                                                                                                                                                       Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3688, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3688
LENGTH: 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                Local Similarity
les 19; Conserv
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                          84.8%; Score 17.8; 90.5%; Pred. No. 9.
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US-10-108-605-44
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US-09-942-310-1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-747-538-1
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                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Broadus, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: AMPLIFICATION BASED POLYMORPHISM
TITLE OF INVENTION: DETECTION
FILE REFERENCE: 6652.US.O1
CURRENT APPLICATION NUMBER: US/09/747,538
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1.0
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Best Local :
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LENGTH: 9432
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44,
                                                                                                                                                                                                                                                                                                                                                                                         Patent No. US20020160934A1
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                                                                                                                          APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
TITLE OF INVENTED TO THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/942,310 CURRENT FILING DATE: 2001-08-29 PRIOR APPLICATION NUMBER: GB 0021286.0 PRIOR FILING DATE: 2000-08-30 NUMBER OF SEQ ID NOS: 77 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Risinger, Carl
APPLICANT: Andersson, Maria K.
APPLICANT: Lewander, Tommy
APPLICANT: Olaisson, Erik
TITLE OF INVENTION: Detection of CYP2D6 Polymorphisms
FILE REFERENCE: GG119.1US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Huff, Jes
APPLICANT: Yu, Hong
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Gentile-Davey,
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Pred. No. 9
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; Sequence 10636, Application US/09960352
; Patent No. US20020137139A1
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NUMBER OF SEQ II
SEQ ID NO 10636
LENGTH: 256
TYPE: DNA
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Best Local Similarity
Matches 18; Conserv
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SEQ ID NO 44
LENGTH: 1157
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                                                                       APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Wathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US/09/335,409
PRIOR FILING DATE: 1999-06-17
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
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NUMBER OF SEQ ID NOS: 361
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Zirkle, Ross
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Pred. No. 46;
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Pred. No. 29;
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 46-LIB188-004-Q1-E1-D10
US-09-960-352-10636
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; OTHER INFORMATION: Clone ID: 11-LIB3058-014-Q1-K1-C3
US-09-960-352-2434
                                                                                                                                           ; SEQ ID NO 10478;

; LENGTH: 422;

; TYPE: DNA

; ORGANISM: BOS taurus

; OTHER INFORMATION: Clone ID: 45-LIB3058-014-Q1-K1-D2

US-09-960-352-10478
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US-09-960-352-2434
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SEQ ID NO 2434
LENGTH: 348
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Best Local
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Best Local
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                                                                                                                                                                                                                                                  APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION.
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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200
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Local Similarity 94.4%;
les 17; Conservation
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TGAGCAAGAACTCGCTGG 217
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17; Conser
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94.48;
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Pred. No. 40;
0; Mismatches
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Pred. No. 39;
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Pred. No. 41;
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; TYPE: DNA; ORGANISM: Bos taurus; OTHER INFORMATION: Clone ID: 56-LIB3058-047-Q1-K1-F12 US-09-960-352-13143
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Best Local Similarity
Thes 18; Conserv
RESULT 11
US-09-960-352-4253
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US-09-960-352-13143
                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: 61-LIB3058-040-Q1-K1-H2
US-09-983-965-4246
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LENGTH: 385
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APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                   SEQ ID NO 4246
LENGTH: 398
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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Warren, APPLICANT: Tao, No
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5912
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                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                     363 GCGTGGGCAAGAGCGCTCTGG
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nes 18; Conserv
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Pred. No. 51;
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Sequence 4253, Application US/09960352 Patent No. US20020137139A1

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US-09-764-864-769/c
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APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEG ID NOS: 15112
SEG ID NO 4253
LENGTH: 452
TYPE: DNA
TYPE: DNA
                                  NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5830
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NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 769
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                                                                    APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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TYPE: DNA
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OTHER INFORMATION: Clone ID: 18-LIB34-086-Q1-E1-E5
                   ENGTH: 454
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Pred. No. 52;
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Query Match
Best Local Similarity
Thes 18; Conserve
                                                                               ; ORGANISM: Homo sapiens US-09-962-832-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Homo sapiens US-09-764-864-354
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US-09-764-864-354/c
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                                                                                                             SEQ ID NO 224
LENGTH: 1443
TYPE: DNA
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SEQ ID NO 354
LENGTH: 498
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APPLICANT: Rosen et
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Best Local Similarity
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                                                                                                                                                                                                                                                      FILE REFERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                    APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-09
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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LOCATION: (181),(244),(385)
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25-LIB3058-057-Q1-K1-G1
                               Score 16.2;
Pred. No. 59;
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Pred. No. 53
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Pred. No. 52;
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Search completed: March 23, 2003, 17:17:27 Job time : 22.5425 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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	2774	53 EP(2)	Bm375926 EBem06_SQ	BE654600 UI-M-AJ1-	AA023366 mh71g05.r	BF524549 UI-R-AE0-	EST57570	LMAJFV1_	T7 end	RE37	вл49	H217	H030	M033	BJ01	J47	Mus	BM555453 AGENCOURT	BG743095 602634230	BQ951805 AGENCOURT	BG775066 602650030	вм048293 603625501	BF384010 602045538	BI144949 602909601	583	BI247531 602960169	892	BI331932 602984323	RH74685.	AV689087 AV689087	AV689088 AV689088	AV692927 AV692927	RE46661.	RH43	F871691 CM4-E3	37426 784	71148 BE87114	вЕ696122 МК1-СТ025

ALIGNMENTS

AW656952 109489 MA AA723009 zh30e05.s AI497811 tm89f05.x BB648303 BB648303 BG699685 602681338 BQ887987 AGENCOURT Description RESULT 1
AW656952
LOCUS
DEFINITION
ACCESSION
VERSION JOURNAL MEDLINE COMMENT REFERENCE AUTHORS SOURCE KEYWORDS TITLE ORGANISM AW656952 448 bp mRNA linear 109489 MARC 1BOV Bos taurus cDNA 5', mRNA sequence. AW656952 AW656952.1 GI:7422778 EST. 1 (bases 1 to 448)
Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett, G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Tel: 402 762 4366 Fax: 402 762 4390 Genome Res. 11 (4), 626-630 (2001) 21180013 Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, Us Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos. .Bos taurus Single pass sequencing. Bases called and alt_trimmed with phred Keele, J.W. Email: smith@email.marc.usda.gov USA EST 25-APR-2001

Result

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Score

Match

Length

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SUMMARIES

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AW656952 AA723009 AI497811 BB648303 BG699685

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Best Local :
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                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2530e05.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone LWAGE:413600 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                  White, Y., Wylie, T., Watersto WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                       est@watson.wustl.edu
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/db_xref="taxon:9913"
/dlone_lib="MARC 1BOV"
/tissue_type="pooled"
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/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/ibrary made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
a 142 c 138 g 72 t
                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:413600"
                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:1305294"
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similar to |
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1 (bases 1 to 470)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Onpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/lmage/lmage.html

Insert Length: 721 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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                                                                                                       adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fatima Bonaldo."

a 155 c 155 g 68 t 1 others
                                                                                                                                                                                                                                         (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. " 66 t
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of captrapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tzawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sakai,K., Ohno,H., Sasaki,O., Shido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KOndo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      e mouse tissues.
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                                /lab_host="DHIOB"
/note="cit--
                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C130007J02"
                         /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                         /tissue_type="head"
/dev_stage="16 days
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                                                                                                                                                         /sex="mixed"
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and sequenced in Mouse Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 664)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                               /note="Organ: brain; Vector: pBluescriptR (modified pBluescript RS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag p): Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                  Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified pBluescript KS(+) after bulk excision from Lambda
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                                                                                                                                                                                                                          /clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                           /clone="IMAGE:4814337"
                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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GCGTGGGCAAGAGCTCGCTGG
                  Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                               BE696122.1
EST.
                                                                                                                                                                              MR1-CT0258-040700-002-f04
                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                           BE696122
                                                                                                                                                                                                        BE696122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 838)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ887987 838 LAGENCOURT_8742650 NIH_MGC_129 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://image.llnl.gov
Plate: LLAM13878 row: g column:
High quality sequence stop: 398.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: ResGen, Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5', mRNA sequence.
BQ887987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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illarity 95.2%;
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/note="Organ: olfactory epithelium; Vector:
/note="Organ: olfactory epithelium; Vector:
/note="Organ: olfactory epithelium; Vector:
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/note="Organ: olfactory epithelium; Vector: olfactory epithelium; Vector:
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/note="Organ: olfactory epithelium; Vector: olfactory epithelium;
Eutheria;
1 to 659)
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/clone_lib="NIH_MGC_129"
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/db_xref="taxon:10090"
                                                                                                                                    GI:10083282
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                  Chordata;
Primates;
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Pred. No. 1.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Score 19.4; DB 14;
Pred. No. 2.1e+02;
0; Mismatches 1;
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CT0258
           Cṛaniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Mus musculus cDNA clone IMAGE:6390947
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2.1e+02;
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                                                                                                                                                                          Homo sapiens cDNA,
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; Murinae; Mus
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GTGGGCAAGAACTCGCTGG
Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakazime,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                          1 (bases 1 to 349)
Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hiranoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,Y., Ito,M., Kawai,J., Koiima,Y., Konno u "......"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-MR1-CT0258-040 700-002-f04&t3-2000-07-04&t4-1) seq primer: puc 18 forward High quality sequence stop: 599.
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                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory of Cancer Genetics Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN full-length enriched, cDNA clone G630027D18 5', m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-*Torgan: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/clone_lib="CT0258"
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78464 MARC 1BOV E
AW437426
AW437426.1 GI:69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., It, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsut
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                                                                                   Bos taurus
                                                                                                                                           COW.
                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Ronno, Fukunishi, Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Ja
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  (bases 1 to
th, T.P.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dev_stage=16 days neonate, sex=mixed),
  (tissue_type=cerebellum, dev_stage=0 day neonate,
    sex=mixed),  (tissue_type=hippocampus, dev_stage=adult,
    sex=male),  (tissue_type=whole body, dev_stage=9 days
    embryo, sex=mixed),  (tissue_type=lung, dev_stage=13 days
    embryo, sex=mixed)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G630027D18"
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                         1 to 368
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90.5%;
Grosse, W.M., Freking, B.A.,
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Pred. No. 8.1e+02;
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  Roberts, A.J., Stone, R.T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single pass sequencing. Bases call v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle
                                         Rua Prof. Antonio Prudente 109,
                                                            Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                   Contact: Simpson A.J.G
                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                           Simpson, A.J.
                                                                                                                                                                                                                            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deollveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                               Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S.,
                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 378)
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EST.
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Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
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Fax: 402 762 4390
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PO Box 166, Clay Center, NE 68933-0166, USA
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                                                                                                                                                                  sequence tags
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Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
123 c 118 g 66 t
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/lab_host="DH10B"
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/clone_lib="MARC 1BOV"
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                                                                                                                                            Acad. Sci. U.S.A.
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                                                                                                                                                                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003684: arm:3R [5513047,5732625]
estimated-cyto:85E6-85F2: 08/18/2001
plate: RH.437 row: E column: 7
                                                                                                                                                                                                                                                                                    Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Stapleton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                           BDGP/HHMI RH Drosophila EST Project
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                                                                                                                                            High quality sequence stop: 450.
                                                                                                                                                                                                                                                                      Fax: 510 486 6798
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BI614393
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-ET0096-
011100-400-f10&t3=2000-11-01&t4=1)
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High quality sequence stop: 225.
Location/Qualifiers
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    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH43755"
/clone_lib="RH Drosophila melanogas
                                                                                                                      ocation/Qualifiers
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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BI362167
BI362167.1 GI:15058195
        l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AB003684: arm:3R [5513047,5732625]
estimated-cyto:8526-85F2:05/13/2001
Plate: RE.466 row: F column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BDGP/HHMI RE Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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                                                                                                              /note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
                                                                                                                                                                                                                       /sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RE46661"
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                                                                                                                                                                                                                                                                                                        /clone_lib="RE Drosophila melanogaster normalized Embryo
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/dev_stage="Adult"
/lab_host="DH5-alpha_TonA"
                             84.8%;
90.5%;
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Pred. No. 8.8e+02;
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AV689088
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
                                                                                                                                              AV689088
AV689088.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chinese National Human Genome Center at Shanghal 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghal 201203, P. R. China Tel: 86-21-50801919(ex.45)
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AV692927 GKC Homo sapiens
AV692927
                                                               Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
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                                                                                              Homo sapiens
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This clone is available at CHGC
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19; Conservative
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                                                (bases 1 to 590)
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                                                                                                                                                                            590 bp mRNA linear EST 16-JAN-2 GKC Homo sapiens cDNA clone GKCDZB06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="hepatocellular
/dev_stage="Adult"
/lab_host="SOLR"
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/db_xref="taxon:9606"
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003 5', mRNA sequence.
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Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                               Contact: Zeguang Han
Chinese National Human Genome Cent
351 Guo Shoujing Road, Zhangjiang
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Zeguang Han Chinese National Human Genome Center at Shanghai Stall Human Genome Center at Shanghai Stall Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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                                                                                                                                              Email: hanzg@chgc.sh.cn
This clone is available at CHGC
                                                                                                                                                                                        201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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This clone is available at
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CC treatment (MDDT) polypeptide (I) selected from a polypeptide having a CC sequence selected from 254 sequences (ABDT21-ABP51844) given in the CC specification, a naturally occurring polypeptide comprising a sequence CC immunogenic fragment of (I). (I) or a biologically active or CC immunogenic fragment of (I). (I) is useful for screening a compound that CC specificatly binds (I) or modulates the activity of (I), and for CC preparing a polyclonal or monoclonal antibody by hybridoma technology. CC Nucleic acids (II) (AB072449-AB072700) encoding (I) are useful for CC screening a compound for effectiveness in altering expression of a target CC polynucleotide comprising. Oligonucleotides and antibodies are useful for CC detecting MDDT in a sample or for assessing toxicity of a test compound, CC in a diagnostic test for a condition or a disease associated with the CC expression of MDDT in a biological sample, for detecting (I) an associated with decreased or increased expression of functional MDDT. (I) or (II) are useful for treating a disease or condition CC associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, associated with aberrant expression of MDDT, where the disorders are cirrhosis, hepatitis, psoriasis, and cancer and an CC autoimmune/inflammatory disorder such as AIDS, Addison's disease, cirrhosis, hepatitis, psoriasis, and cancer and an CC allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or rheumatoid arthritis. (II) are useful for creating knockin humanised or type, for detecting differences in the chromosomal location due to CC and as hybridisation probes for mapping naturally occurring genomic CC and as hybridisation probes for mapping naturally occurring genomic
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Bradley DL, Rohatgi SD, Harris B, Roseberry
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                                                                                                                                                                228
                                                                                                               .8e-103;
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RESULT 2
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06-SEP-2000;
                                                                                                                                                                                                                                                  proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autolimnune disorder; inflammatory disorder, allergy; multiple scleros; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigo
                                                                                                                                              06-SEP-2001;
                                                                                                                                                                                            WO200240715-A2
                                                                                                                                                                      23-MAY-2002
                                                                                                                                                                                                                                          neuroprotective;
                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                     Human MDDT encoding
                                                                                                                                                                                                                                                                                                                                                               03-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                          ABQ72648 standard; cDNA; 3061
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                                                                                                                                                                                                                                                                                                                MDDT; disease detection
2000US-230515P.
2000US-230514P.
2000US-230517P.
2000US-230519P.
2000US-230518P.
2000US-230559P.
2000US-23059P.
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2000US-23059P.
2000US-23059P.
2000US-23059P.
2000US-23059P.
                                                                                                                                             2001WO-US27628
                                                                                                                                                                                                                                        antirheumatic; antiarthritic; gene;
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tis; psoriasis; cancer; AIDS;
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                                                                                                                                                                                                                                                                                       sclerosis;
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                                                                                                                                                                                                                 CC The invention relates to an isolated human disease detection and CC treatment (MDDT) polypeptide (I) selected from a polypeptide having a CC sequence selected from 254 sequences (ABP51231-ABP51484) given in the CC specification, a naturally occurring polypeptide comprising a sequence CC immunogenic fragment of (I). (I) is useful for screening a compound for CC immunogenic fragment of (I). (I) is useful for screening a compound that CC specifically binds (I) or modulates the activity of (I), and for CC greparing a polyclonal or monoclonal antibody by hybridoma technology. CC Nucleic acids (II) (ABC72449-ABC72700) encoding (I) are useful for CC screening a compound for effectiveness in altering expression of a target CP polynucleotide comprising. Oligonucleotides and antibodies are useful for CC and for purifying (I) from a sample or for assessing toxicity of a test compound. CC in a diagnostic test for a condition or a disease associated with the CC expression of MDDT in a binlogical sample, for detecting (I) in a sample, associated with decreased or increased expression of functional MDDT. CC associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, criminals or transgenic animals, asthma, atherosclerosis, and cancer and an autoimmune/inflammatory disorder such as AIDS, Addison's disease, animals or transgenic animals to model human diseases, in somatic or cell type, for detecting differences in the chromosomal location due to canda subtraction among normals, carrier or affected individuals or canda an animals or transcript image of a tissue or cell candas bubridies for maching normals or conditionals individuals.
                                                                                                                                                                    Query Match
Best Local
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06-SEP-2000;
06-SEP-2000;
07-SEP-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g. AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones AL, Yu
Momiyama MG,
                                                                                                                                                                                                                 Sequence 3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page
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                                                                                                                                                                                                                                                              as hybridisation
                                                                                                        ATGCCGGAACAGAGTAACGATTACCGCGTGGTGGTGTTCGGGGCGGCGGCGGCGTGGGCAAG
GAGGACACCTACCGGCAGGTGATCAGCTGCGACAAGAGCGTGTGCACGCTGCAGATCACA
                                                 AGCTCGCTGGTGCTGCGCTTCGTGAAGGGCACGTTCCCGCGACACCTACATCCCCACCATC
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; 2000US-230988P.
; 2000US-230989P.
; 2000US-230951P.
; 2000US-231163P.
; 2000US-231167P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          u JY, Wright RJ, Gietzen D, Liu Bradley DL, Rohatgi SD, Harris I Peralta CH, David MH, Panzer SR,
                                                                                                                                                    Conservative
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                                                                                                                                                                                                                 BP;
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Pred.
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No. 2.4
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                                                                                                                                                                                 24;
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u TF, Yap PE, F
s B, Roseberry I
                                                                                                                                                    Indels
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 180
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Tang Wang Zhao

οΑ, QA,

Liu ( Wang ; Zhou

Wehrman Asundi V,

Chen R, ž

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Drmanac Ç

Xue Y, AJ, RT;

Qiạn XB, Yang Y,

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Wang

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WPI; 2001-442253/47 P-PSDB; AAM41682.

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                                                                                                                 09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; hemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukharmis.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAI60838 standard; cDNA; 1087
                                                                                              19-OCT-2000;
29-NOV-2000;
                                                                                                                                                              21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                              26-DEC-2000;
                                                                                                                                                                                                                    26-JUL-2001.
                                                                                                                                                                                                                                          WO200153312-A1
                                                                                                                                                                                                                                                               Homo
                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                     _eukaemia; ss.
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                                                                                                                                                                                                                                                                                                                                                               polynucleotide
                                                                         HYSEQ
                                                                                            2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0652191.
2000US-0652191.
2000US-0639036.
2000US-0727344.
                                                                                                                                                                                              2000WO-US34263
                           u P,
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                                                                         INC
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                                                                                                                           CGCACATGGAAGTGTGCCTTCATGGAGACCTCAGCCAAGCTCAACCATAACGTGAAGGAG
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AAAAAGAGCAAGCAGCAGAAAAGGAAAGAGAAGCTCAAAGGCAAGTGCGTGATCATGTGA
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78.3%;
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Pred. No. 1.6e-64;
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RESULT 4 AAI59052 ID AAIS

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14-SEP-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                             in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropaths and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, hemotactic/chemokinetic activity, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nervous system; neuropathy; central nervous system; Calzheimer's; Parkinson's disease; Huntington's disease; haemosta amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                   Sequence 1108
                                                                                                                                         C.N.S disorders.
Note: The sequence data
                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                            specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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172
             1 ATGCCGGAACAGAGTAACGATTACCGCGTGGTGGTGTTCGGGGCGGCGGCGGCGGCGAAG
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ATGCCTGAGCAGAGTAACGATTACCGGGTGGCCGTGTTTTGGGGCCTGGCGGTGTTTGGCAAG
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                                                              Similarity
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Zhou P,
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2000US-0598042
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Wehrman T, X
Goodrich R,
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                                                                                                                                                                                                                                                                     Human; intracellular signalling; INTSIG-16; gene therapy; nausea; asthma; Crohn's disease; keratosis; cell proliferative disorder; Grave's disease; arteriosclerosis; hepatitis; leukaemia; autoimmune disorder; meningitis; acquired immunedeficiency syndrome; AIDS; allergy dermatitis; psoriasis; Hashimoto's thyroiditis; neurological disorder; developmental disorder; gastrointestinal disorder; reproductive disorder; nootropic; antiemetic; Alzheimer's disease; dementia; Creutzfeldt-Jacob disease; dermatological; antiinflammatory; anaemia; nephrotropic; immunosuppressive; thyromimetic; cancer; neuroprotective; cerebroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                          gynaecological;
                                                                                                     mat_peptide
                                                                                                                                   sig_peptide
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                                                                                                                                                                                                                               Homo
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                                            WO200231152-A2
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161..259
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260..757
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161..760
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13-OCT-2000;
30-OCT-2000;
15-NOV-2000;
22-NOV-2000;
13-DEC-2000;
                          disorder e.g. keratosis, arteriosclerosis, hepatitis, psoriasis, leukaemia; autoimmune disorders e.g. AIDS, allergies, anaemia, asthma, Crohn's disease, dermatitis, Graves' disease, Hashimoto's thyroiditis; neurological disorders e.g. Alzheimer's disease, dementia, meningitis, Creutzfeldt-Jacob disease; gastrointestinal disorders e.g. nausea, reproductive disorders e.g. menstrual disorders, ectopic pregnancy and cancer of the breast and developmental disorders. The present sequence is human INTSIG-16 cDNA.
                                                                                                                                                  The invention relates to an isolated intracellular signalling (INTSIG) polypeptide or a biologically active or immunogenic fragment of INTSIG. INTSIG is also useful for preparing a polyclonal or monoclonal antibody by hybridoma technology. INTSIG gene is useful in gene therapy. INTSIG is useful for treating or preventing disorders such as cell proliferative
                                                                                                                                                                                                                                                                               Novel intracellular signaling polypeptide useful for treating preventing cell proliferative, autoimmune, neurological, gastrointestinal and reproductive and developmental disorders
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                                                                                                                                                                                                                                                    Claim
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Sequence
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an R, Hafalia AJA, K
Lu Y, Nguyen DB, A
elu K, Thornton M, W
 4167
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2000US-244723P.
2000US-249402P.
2000US-252622P.
2000US-255622P.
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B₽;
1098 A; 911 C;
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Arvizu C, Ramkumar J,
Walia NK, Warren BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VS,
960 G; 1198 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gandhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AR,
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Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
Xu Y, Yac
                                                                                                                                                                                                                                                                                                                                                                                                           Yao
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Query Match

Best Local Similarity

Matches 470; Conserv Conservative 63.8%; 78.3%; 0 Score 380.8; DB 24; Length Pred. No. 1.7e-64; O; Mismatches 127; Indels Length ω •• Gaps

1:

QY В Q 161 61 ATGCCGGAACAGAGTAACGATTACCGCGTGGTGGTGTTCGGGGCGGCGGCGGCGTGGGCAAG ATGCCTGAGCAGAGTAACGATTACCGGGTGGCCGTGTTTGGGGCCTGGCGGTGTTGGCAAG 60

221 AGCTCGCTGGTGCTGCGCTTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATC 120 AGCTCCCTGGTGTTGAGGTTTGTGAAAGGCACATTCCGGGAGAGCTACATCCCGACGGTG

121 281 GAGGACACCTACCGGCAGGTGATCAGCTGCGACAAGAGCGTGTGCACGCTGCAGATCACA 180 GAAGACACCTACCGGCAAGTGATCAGCTGTGACAAGAGCATATGCACATTGCAGATCACC

181 GACACCACCGGCAGCCACTTCCCCGGCCATGCAGCGCCTGTCCATCTCCAAGGGCCAC

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Qy 301 TACAAGCTCATCGTGCAGATCAAGGGCAGCGTGGAGGACATCCCCGTGATGCTCGTGGGC

Š 밁 461 AACAAGTGCGATGAGACGCAG----CGGGAGGTGGACACGCGCGGAGGCGCAGGCCGTGGCC 520

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                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLO1840-ABL18175) and the encoded proteins (ABBS7737-ABB72072).
                                                                                                                                         The sequence data for this patent did not form part of the pri specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL14159 standard;
                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical; gene;
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DB; ABB70056.
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                                                                                                             702
                                                                                                                                                                                                                                                               SEQ ID NO 36959; 21pp + Sequence Listing; English
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                                                                 Conservative
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                                                               ; Score 303.2; I; Pred. No. 1.3e-
0; Mismatches
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                                                                                                         220 G; 110 T; 0 other;
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New guanosine triphosphate-binding encoding nucleic acids, useful for

treating and

ed proteins (GBAP) and/or diagnosing

and their diseases

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23-AUG-1999;
15-OCT-1999;
                                                                                                                                                 Yue H,
Reddy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; guanosine triphosphate binding associated protein; GTP; GBAP; inflammation; AIDS; Addison's disease; anaemia; arteriosclerosis; asthma; autoimmune disorder; hepatitis; multiple sclerosis; cancer; diabetes;
                                                                           P-PSDB; AAB68550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200105970-A2
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Lu DAM, A
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Azimzai Y,
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Patterson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
   Homo
                              Human; primer;
                                                               Human cDNA sequence
                                                                                               26-JUN-2001
                                                                                                                             AAH15447;
                                                                                                                                                           AAH15447 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis, multiple sclerosis, cancer, diabetes, osteoporosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          including inflammation, AIDS, Addison's disease, anaemia, arteriosclerosis, asthma, autoimmune disorders, Grave's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated with GBAP
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                              detection; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 A;
                                                                                                                                                           cDNA;
                                                            SEQ ID NO:13678
                                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 C;
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Pred. No. 5.6e-34;
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                             antisense therapy; gene therapy;
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TGGTGTTCTCCGTCACCAGCAAGCAGTCGCTGGAGGAGCTGGGGCCCATCTACAAGCTCA 310 GTGGCGACGCCAACCGCGCTCTGCAGCGCCACGTTATAGCCCGGGGCCACGCCTTCGTCC GCAGCCACCAGTTCCCGGCCATGCAGCGCCTGTCCATCCCAAGGGCCACGCCTTCATCC 625

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ACCGGCAGGTGATCAGCTGCGACAAGAGCGTGTGCACGCTGCAGATCACAGACACCACCG

ACTGCCAGTTGCTGGGCTGCAGCCACGGTGTGCTTTCCCTGCACATCACCGACAGCAAGA

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TGCTGCGCTTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATCGAGGACACCT 130 AGATCAGAGATTACCGCGTCGTGGTAGTCGGCACCGCTGGTGTGGGGGAAAAGTACGCTGC

 ${ t TGCACAAGTGGGCGAGCGGCAACTTCCGTCATGAGTACCTGCCGACCATTGAAAATACCT}$ 

191

Matches Query Match Best Local

al Similarity 367; Conserv

Conservative

0;

37.2%;

Score 222; Pred. No. !

DB

Length Indels

1561;

ed. No. 5.7e-34; Mismatches 220

220; 22;

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Gaps

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564 70

505

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CC comprises: (a) an oligon-dp primer and an oligonucleotide complementary crand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the cC oligonucleotide comprises at least 15 nucleotides; or (b) a combination (c) of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination (c) of an oligonucleotide comprises a sequence complementary to the cC complementary strand of a polynucleotide which comprises a 5'-end cC complementary to a cplynucleotide which comprises a 3'-end sequence, where the cC oligonucleotide comprises a 1'-end sequence, where the cC oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in cC the specification. The primer sets can be used in antisense therapy and cC in gene therapy. The primers are useful for synthesising polynucleotides, catelotial primers are also useful for the cC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the cC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CAAH3633 to AAH18742 represent human cDNAs sequences; AAAB92446 to AAH3633 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present oligonucleotides, all of which are used in the exemplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly tfull-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs -
 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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   1561 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID 13678;
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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 422 A; 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             2537pp + CD ROM; English
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C; 373 G; 406 T; 0
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A, Nagai K,
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Otsuki
   other;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, use diagnostics, forensics, gene mapping, identification of m responsible for genetic disorders or other traits and to biodiversity
                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 23660; 103pp; English.
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23-AUG-2000;
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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AGATGCCCAACACCACTGAGAAGCTGCTTGACAAGTGCATAATCATGTGA 3403
                                   GGAAGCAGAAGAGGACAGACCGCGTCAAGGGCAAATGCACCCTCATGTGA 597
                                                                         TGCTGCTGAATTACAAGAAAAAGCCCCACCACCGGCCTCCAGGAGCCCGAGAAGAAATCCC
                                                                                                              AGCTGCTGACGCTGGAGACGCCGGAACATGAGCCTCAACATCGACGGCAAGCGCTCCG
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AAV60578 standard; CDNA; 7397

## AAV60578

18-JAN-1999 (first entry)

Human tumour suppressor gene NOEY2.

AAV60578
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AC AAV6
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AC I8-J
DT 18-J
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KW NOEY
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OS Homo diagnosis; gene therapy; NOEY2; tumour suppressor; human; breast cancer; transgenic animal; ovary

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reading frame encodes a 26 kDa polypeptide (see AAW79898) that shows homology to members of the Ras and Rap family. The gene is isolated from human chromosome lp31. A full-length cDNA clone (see AAV60577) is also claimed. NOEY2 nucleic acids can be used in the recombinant production of NOEY2 polypeptides, in the gene therapy of cancer (especially ovarian and breast-related), and to prepare transgenic animals useful as models of cancer. Fragments of NOEY2 nucleic acids are also used as probes and primers for, diagnosis, including detection of mutations, or as antisense molecules or ribozymes for reducing/eliminating NOEY2 activity. The nucleic acids can also be used to screen for antitumour agents that stimulate NOEY2, overcome lack of this protein or block expression of the protein or block expression or the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the NOEY2 gene nucleotide sequence. NOEY2 is a novel tumour suppressor gene that is expressed in normal ovarian and breast surface epithelial cells but is consistently absent or down regulated in ovarian and breast cancer cells. The open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding NOEY2 tumour suppressor from epithelium - useful for, e.g. treatment, diagnosis and cancer, particularly cancer of ovary and breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4;
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21-MAR-1997;
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Pred. No. 1.3e-33;
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RESULT 11
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that shows homology to members of the Ras and Rap family. Differential display PCR was used to isolate and clone the novel gene, and RACE was used to amplify the full-length NOEY2 cDNA from human ovarian surface epithelial cells. A NOEY2 genomic DNA sequence (see AAV60578), isolated from human chromosome 1p31, is also claimed. NOEY2 nucleic acids can be used in the recombinant production of NOEY2 polypeptides, in the gene therapy of cancer (especially ovarian and breast-related cancers), and to prepare transgenic animals useful as models of cancer. Fragments of NOEY2
                                                                                                                                                                         This is the complete NOEY2 cDNA nucleotide sequence. NOEY2 is novel human tumour suppressor gene that is expressed in normal ovarian and breast surface epithelial cells but is consistently
                                                                                                                                                                                                                                                                      New nucleic acid encoding NOEY2 tumour suppressor from ovarian epithelium - useful for, e.g. treatment, diagnosis and prognos cancer, particularly cancer of ovary and breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-1998;
21-MAR-1997;
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                                                                                                                                          absent or down-regulated in ovarian and breast cancer cells. The open reading frame encodes a 26 kDa polypeptide (see AAW79898)
                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-532005/45
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                                                                                                                                                                                                                                         Claim 4; Page 148-150; 182pp; English.
                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                     Bast RC,
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97US-0041580
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Best Local S
Matches 367
                                                             Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic ac including ribozymes acids can stimulate
WO200153453-A2
                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                               AGCTGCTGACGCTGGAGACGCCCCGGAACATGAGCCTCAACATCGACGGCAAGCGCTCCG
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                                                    immunodeficiency virus; HIV; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acids are also used as probes and primers for diagnosis, ng detection of mutations, or as antisense molecules or es for reducing/eliminating NOEV2 activity. The nucleic an also be used to screen for antitumour agents that the NOEV2, overcome lack of this protein or block expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Pred. No. 6.8
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
30-NOV-2000;
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25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coaquiation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1144 BP; 220 A; 314 C; 367 G;
                                                                                                                                                                                                                                                                                                                                                                                                                              chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present seque expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders - {\sf res}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao
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GTGAAGCGGTACGAGCGCGTGCCCATGATCCTGGTGGGCCAACAAGGTGGACCTGGAGGGT
                                                                     TCCGTCACCAGCAGCAGTCGCTGGAGGAGCTGGGGGCCCATCTACAAGCTCATCGTGCAG
                                                                                                                            CAGTTCCCGGCCATGCAGCGCCTGTCCATCTCCAAGGGCCACGCCTTCATCCTGGTGTTC
                                                                                                                                                                                    GTGATCAGCTGCGACAAGAGCGTGTGCACGCTGCAGATCACAGACACCACCGGCAGCCAC
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                          ATCAAGGGCAGCGTGGAGGACATCCCCGTGATGCTCGTGGGCAACAAGTGCGATGAGACG
                                                      AGCCTCGTCAACCAGCAGAGCTTCCAGGACATCAAGCCCATGCGGGACCAGATCATCCGC
                                                                                                               CAGTTCGCGTCCATGCGGGACCTGTACATCAAGAACGGCCAGGGCTTCATCCTGGTCTAC
                                                                                                                                                                     GAGATTGAGGTGGACTCGCCGTCGGTGGTGCTGGAGATCCTGGATACGGCGGGCACCGAG
                                                                                                                                                                                                                              TTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATCGAGGACACCTACCGGCAG
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                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYSEQ INC.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0250583.
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2000US-0552317.
2000US-0598042.
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58.2%;
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24-FEB-2000

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19-MAY-2000

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                      2000US-017905.
2000US-018658.
2000US-01866350.
2000US-018675.
2000US-019874.
2000US-0198123.
2000US-0214886.
2000US-0215135.
2000US-0216847.
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2000US-0232081
2000US-0232398
2000US-0232399
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Best Local Sim
Matches 308;
                                                                                                                                                                                                                                                                                                                                  amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, alagnose and treat immune/haemarcopoletic-related diseases, especially cancers and cancer methaticas of hometic-telated diseases, especially
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01-DEC-2000;
05-DEC-2000;
   4349
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                                                                                                                                                                                                                                                                                        cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic seguences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                                                                               Sequence 4933 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides useful for preventing, diagnosing and/or treating cancers and metastasis -
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06-DEC-2000;
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17-NOV-2000;
                                                                                                                                                                                                                                                                         represent sequences used in the exemplification of the present invention
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                                 139
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                                                                                                                                                                                                   Local Similarity
               TTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATCGAGGACACCTACCGGCAG
                                                                                                                      GAGTACAAAGTGGTGCTGGGCTCGGGCGGCGTGGGCCAAGTCCGCGCTCACCGTGCAG
                                                                                                                                     GAGATTGAGGTGGACTCGTCGCCGTCGGTGCTGGAGATCCTGGATACGGCGGGCACCGAG
                                                           Barash SC,
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; 2000US-0251868.
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2000US-0249297
2000US-0249299
2000US-0249390
2000US-0250160
2000US-0250160
2000US-0250198
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2000US-0249216.
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Pred. No. 5.5
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                             26-JUL-2000;
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cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                       immune;
                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                    2000US-0220963.
2000US-0220964.
2000US-0224518.
2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-019076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0211886.
2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-02174887.
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                              2000US-0225266
2000US-0225267
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2000US-0218290
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                                                                                                                                                                                                                                                                                                                                                                                                                       haematopoietic;
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ine; metastasis; ds.
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26-SEP-2000

27-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

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29-SEP-2000

02-OCT-2000

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06-NOV-2000

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21-SEP-2000;
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22-AUG-2000;
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23-AUG-2000;
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25-SEP-2000;
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2000US-0225757

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2000US-02258681

2000US-02268681

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2000US-0229892

2000US-0229343

2000US-0229345

2000US-0229513

2000US-0229513

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2000US-0231413

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2000US-0233491

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2000US-0246528
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                                                                                                                                                                                                                                                                                       CA,
                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                       Barash
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2000US-0246611.
2000US-0246611.
2000US-02449209.
2000US-0249210.
2000US-0249211.
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2000US-0249211.
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2000US-0249214.
2000US-0249216.
2000US-0251030.
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                                                                                                                                                                                                                                                                                        SC,
                                                                                                                                                                                                                                                                                                            SCI INC
                                                                                                                                                                                                                                                                                        Ruben
                                                                                                                                                                                                                                                                                       SM;
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Nucleic acids encoding useful for preventing, metastasis metastasis human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and

Disclosure; SEQ ID No 36046; 3071pp + Sequence Listing; English

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic corrected strom the present invention. AAK54942 to AAK8793 and AAM82169 CC expressent servences used in the exemplification of the prevent in the present invention. sequences used in the exemplification of the present invention the and

Sequence 4934 B₽; 1542 Α; 1175 C; 985 G; 1232 Τ, 0

Query Match
Best Local Similarity
Matches 308; Conserv Conservative 29.4%; 58.2%; 0, Score 175.4; Pred. No. 5.5 Mismatches . 5e DB 22; Indels Length 4934; 0; Gaps 0

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RESULT 15
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DNA encoding sequences associated with human oncogenes - and derived antibodies, useful for in vitro diagnosis of cancer and for therapy.
                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                             RAP2 Gene encoding at least one peptide associated with ras oncogene.
                                            WPI; 1990-037122/05.
P-PSDB; AAR05076.
                                                                                                                                             04-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                   AAQ03212 standard;
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                                                                            Tavitian A, Pizon V,
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                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGAGACCTCGGCCAAGATGAACTACAACGTCAAGGAGCTCTTCCAGGAGCTGCTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGCGCGAGGTCTCGTACGGGGAGGGGCAAGGCCCTGGCTGAGGAGTGGAGCTGCCCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCGGGAGGTGGACACGCGCGAGGCGCAGGCGGTGGCCCAAGAGTGCAAAGTGCGCTTTC 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTTCCCGGCCATGCAGCGCCTGTCCATCTCCAAGGGCCACGCCTTCATCCTGGTGTTC
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                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                              cancer;
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Search completed: March Job time: 709.666 secs

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 558 BP; 142 A; 143 C; 165 G; 108 T; 0 other;
489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3a-b; 92pp; French.
                                  498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 CTTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATCGAGGACACCCTACCGGCA 137
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                                                                                                                                         GCAGCGGGAGGTGGACACGCGCGGAGGCGCAGGCGGTGGCCCAAGAGTGGAAGTGCGCTTT
                                                                                                                                                                                                                    GATCAAGGGCAGCGTGGAGGACATCCCCCGTGATGCTCGTGGGCAACAAGTGCGATGAGAC
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   GCAGATGA
                                GCTGGAGA 505
                                                            TATGGAAACTTCCGCTAAGAGTAAAACAATGGTGGACGAACTCTTTGCAGAAATTGTGAG
                                                                                                                          TGAGAGAGAAGTATCGTCCAGCGAAGGCAGAGCCCTTGCTGAAGAGTGGGGGCTGCCCCTT
                                                                                                                                                                                        CGTGAAGCGGTATGAGAAAGTGCCAGTCATCTTGGTTGGGAACAAAGTGGACCTGGAAAG
                                                                                                                                                                                                                                                    CAGCCTCGTCAACCAGCAGAGCTTCCAGGACATCAAGCCCATGCGGGACCAGATCATCCG
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   496
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                                                                                                                                                                                               AUTHORS
TITLE
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10709 row: k column: 10
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                          Mammalia; Eutheria;
1 (bases 1 to 664)
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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          Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs t
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.
Watahiki,M., Yoneda,Y., Ishkawa,T., Ozawa,K., Tanaka,T., Mats
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sug,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Unpublished (2001)
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            144
                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken
                               FLC
                                                                                                                                                                                     contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                  modified pBluescript
                                                                   cap-trapper. Second strand cDNA was
primer adapter of sequence {5'
                                                                                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length
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/lab_host="DH10B"
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/clone="C130007J02"
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                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="mixed"
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/strain="C57BL/6J"
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16 days embryo

Izawa,M., Ohara,E., K., Tanaka,T., Matsu

Matsuura

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                                                   NIH-MGC http://mgc.nci.nih.gov/.
NAIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MG Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
             found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM13878 row: g column: 12
                                                                                                                                                                                                                                                                                                                      AGENCOURT_8742650 NIH_MGC_1295', mRNA sequence.
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similar to
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AI497811
AI497811.1
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: olfactory epithelium; Vector:
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/note="Organ: olfactory epithelium; Vector:
/note="Organ: olfactory epithelium; Vector:
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/clone="IMAGE:6390947"
/clone_lib="NIH_MGC_129"
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Pred. No. 1.3e-81;
""" matches 79;
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           AACAAGTGCGATGAGACGCAGCGGGAGGTGGACACGCGCGAGGGGGGAGGCGCTGGCCCA 419
                                         TACAAGCTCATCGTGCAGATCAAGGGCAGCGTGGAGGACATCCCCGTGATGCTCGTGGGC
                                                                                                                                       GACACCACCGGCAGCCACCAGTTCCCGGCCATGCAGCGCCTGTCCATCTCCAAGGGCCAC
                                                                                         GCCTTCATCCTGGTGTTCTCCGTCACCAGCAAGCAGTCGCTGGAGGAGCTGGGGGCCCATC
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                                                                                                                                                                                       GAGGACACCTACCGGCAGGTGATCAGCTGCGACAAGAGCGTGTGCACGCTGCAGATCACA 180
                                                                                                                                                                                                                                                  AGCTCGCTGGTGCGCTTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATC 120
                                                                                                                                                                                                                                                                                      1 (bases 1 to 470)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAl Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-bio.llnl.gov/bbrp/1mage/1mage.html
Insert Length: 721 Std Error: 0.00
Seq primer: -40Up from G1bco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 455.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                  91
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2165313"
/clone=lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                 Score 416.4;
Pred. No. 5.
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Local Similarity
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                                                                                                                GACACCACCGGCAGCCACCAGTTCCCGGCCATGCAGCGCCTGTCCATCTCCAAGGGCCAC 240
                                                                                                                                                                                                                                                      AGCTCGCTGGTGCTGCGCTTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATC 120
                                                                                                                                                                                                                                    AGCTCGCTGGTGCTGCGCTTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATC
                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 453.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of 4444 Forest Park Parkway, Box Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Wilson RK
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1 (bases 1 to 454)
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AA723009
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/clone="IMAGE:413600"
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/db_xref="GDB:1305294"
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99.8%;
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Pred. No. 3.
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Fax: 319 335 9565
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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UI-R-BU0-aoz-h-08-0-UI.sl UI-R-BU0 Rattus norvegicus
UI-R-BU0-aoz-h-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
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/db_xxef="taxon:10116"
/clone="U1-R-BU0-aoz-h-08-0-UI"
/clone_1ib="U1-R-BU0"
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                                                    UI-R-BU0-apd-d-07-0-UI.Sl UI-R-BU0 Rattus norvegicus UI-R-BU0-apd-d-07-0-UI 3', mRNA sequence.
         Norway rat.
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REFERENCE AUTHORS FEATURES COMMENT JOURNAL MEDLINE TITLE source Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa Tel: 319 335 8250
Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in be
is likely internal to the message. cDNA Library
Soares Lab Clone distribution: clones will be av Normalization and subtraction: two discovery Genome Res. 6 (9), 791-806 (1996) 1 (bases 1 to 456) Bonaldo, M.F., Lenno Contact: Soares, 97044477 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; POLYA=No Research Genetics (www.resgen.com) Rattus primer: /lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BU0
library is a subtracted library derived from a mixture of
eye and ganglia tissues. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest.eng.uiowa.edu. The subtraction has /clone="UI-R-BU0-apd-d-07-0-UI" /clone_lib="UI-R-BU0" /dev_stage="adult" /strain="Sprague-Dawley /organism="Rattus norvegicus" Location/Qualifiers /db_xref="taxon:10116" M13 Forward Lennon, G. and Soares, M.B. approaches City, Muridae; beginning of sury Preparation: available through ç facilitate Ā EST 12-JUN-2000 Murinae; of sequence gene ъ.

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                                                           Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa Tel: 319 335 8250 Fax: 319 335 9565
       Email: msoares@blue.weeg.uiowa.edu
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is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
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Bonaldo, M.F., Lenno
Normalization and s
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Rattus norvegicus
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UI-R-Y0-abj-f-09-0-UI 3',
Research Genetics (www.resgen.com)
                                                                                                                            Contact: Soares,
                                                                                                                                          97044477
                                                                                                                                                    Genome Res. 6 (9),
                                                                                                                                                                  discovery
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae.
                                                                                                                                                                                                                                                                                             AI764459.1
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TAG_SEC-None found"
142 c 140 g 108 t
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89.9%;
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                                                                                                                                                    791-806 (1996)
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UI-R-YO Rattus norvegicus
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CDNA clone
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                                                    AGACGCGCGGGAACATGAGCCTCAACATCGACGGCAAGCGCTCCGGGAAGCAGAAGAGGA
                                                                                                                                          AGACCTCGGCCAAGATGAACTACAACGTGAAGGAGCTGTTCCAGGAGCTGCTGACGCTCG
                                                                                                                                                                                    AGACCTCGGCCAAGATGAACTACAACGTCAAGGAGCTCTTCCAGGAGCTGCTGACGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCAGCCATGCAGCGGCTGTCCATCTCCAAGGGCCACGCCTTCATCCTGGTGTTCTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="vector: pT773D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-YO library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-EO, UI-R-EI, UI-R-CO, and UI-R-CI). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-YO) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3: ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-YO library. This procedure has been previously described.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_LIB=UI-R-Y0
TAG_TISSUE=Eye
TAG_SEQ=CATTG"
a 133 c 128
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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1996)
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299
               CCAGCAAGCAGTCGCTGGAGGAGCTGGGGGCCCATCTACAAGCTCATCGTGCAGATCAAGG 325
                                                                                        CGGCCATGCAGCGCCTGTCCCATCTCCCAAGGGCCACGCCTTCATCCTGGTGTTTCTCCCGTCA 265
                                                                                                                                         a
CCAGCAAGCAGTCGCTGGACGAGCTGAGCCCCATCTACAAGCTGATCGTGCAGATCAAGG
                                                                   CAGCCATGCAGCGGCTGTCCATCTCCAAGGGCCACGCCTTCATCCTGGTGTTTCTCGGTGA 300
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419 bp mRNA linear IUI-R-BU0-anb-f-04-0-UI.sl UI-R-BU0 Rattus norvegicus UI-R-BU0-anb-f-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        discovery
Genome_Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Normalization and subtraction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus.
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                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BUO
library is a subtracted library derived from a mixture of
eye and ganglia tissues. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest.eng.uiowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                         TAG_TISSUE=ganglia
TAG_SEQ=GCAGAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UI-R-BU0-anb-f-04-0-UI"
/clone_lib="UI-R-BU0"
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/db_xref="taxon:10116"
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89.7%;
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Rodentia;
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Pred. No. 1.7e
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GCAGCGTGGAGGACATCCCCGTGATGCTCGTGGGCAACAAGTGCGATGAGACGCAGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sl
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 801)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG702913.1
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                                                                                                                                                                                                                                                                                                                                                                                         http://image.llnl.gov
Plate: LLAM10717 row: d column:
High quality sequence stop: 760.
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Contact: Robert Strausberg, Ph.D.
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                                           Conservative
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                                                                                                                   b
                                                                                                              /tissue_type="hippocampus"
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                                                                                                                                                                                                                                                                                             /clone="IMAGE:4817247"
/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                      56.9%;
78.3%;
                                        0,:
                                       Score 339.4; DB 12;
Pred. No. 1.7e-58;
0; Mismatches 121;
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152 ATGCCTGAGCAGAGTAACGATTACCGGGTGGCCGTGTTTGGGGCTGGCGGTGTTGGCAAG 211

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                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; v
Mammalla; Eutherla; Primates; Catarrhini;
1 (bases 1 to 645)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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603191841F1 NIH_MGC_95
                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL http://lmage.llnl.gov
                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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                                                                                                                 quality sequence stop: 634.
                                                                                                                                LLAM11663 row: a column:
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/clone=lib="NIH_MGC_95"
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                                                                                               Location/Qualifiers
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AW305720.1
1 (ba
                   Danio rerio
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
                                                                                             AW305720 702 bp mRNA 11 fj63a05.y1 zebrafish adult brain Danio rerio TR:095057 095057 BC41195_1.;, mRNA sequence.
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1 to 702)
Johnson, S.
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79.9%;
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                           Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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Lehrach, H.,

Lee,

Li, F.,

Marra, M.,

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BASE COUNT
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GAGTGGAAGTGCGCTTTCATGGAGACCTCGGCCAAGATGAACTACAACGTCAAGGAGCTC 480
                                                                                                                                                                                                                                                          TACCAGCAAGTGCTGGCCATCAAAGGCAACGTGGAGAACATCCCCCATCATGCTTGTGGGT 579
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                                                                                   AACAAGAGCGATGAGACCCAGCGCGAGGTGGAGACCAAGGATGGCGAGGCTCANGCAAAC 639
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cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwoo,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
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Location/Qualifiers
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/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
/note="Vector: pZIPLOX; Site_1: NotI; Site_1: NotI; Site_2: SalI;
/note="Vector: pZIPLOX; Site_1: NotI; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="brain"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="zebrafish adult brain"
/sex="mixed male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/db_xref="taxon:7955"
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Pred. No. 2.8e
0; Mismatches
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                                                                                                                                   GAGCTCGCTGGTGCTGCGCTTCGTGAAGGGCACGTTCCGCG-ACACCTACATCCCCACCA 118
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                                     TGGAAGACACCTACCGGCAAGTGATCAGCTGTGACAAGAGCATATGCACATTGCAGATCA
                                                                                                                 GAGCTCCCTGGTGTCGAGGTTCGTGAAAGGCACATTCCGGGCAGAGCTACATCCCGACGG 193
                                                                         TCGAGGACACCTACCGGCAGGTGATCAGCTGCGACAAGAGCGTGTGCACGCTGCAGATCA 178
                                                                                                                                                                                                                                                                         469;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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603195901F1 NIH_MGC_95 Homo
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Location/Qualifiers
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Plate: LLAM11695 row: b column:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                   for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Li constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Li a 228 c 238 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Salt-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
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/clone="IMAGE:5275297"
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77.3%;
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                                                                                                                                            This read has been produced as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having 100 or more base pairs with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For information on obtaining this clone, please contact
                                                                                                                                                                                                                                                             resequencing for verification Unpublished (2001) Contact: Prange CK The I.M.A.G.E. Consortium
                                                                                                                         info@image.llnl.gov.
Plate: LLAM10715 ro
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1mageqc_4_2001/smu47bdff41.x1

IMAGE:4816673 5', mRNA sequeno

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Email: help@image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                    Lawrence Livermore National Laboratory
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BM172422.1
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                                                                                     quality sequence stop: 628
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4816673"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
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                     GCTCTTCCAGGAGCTGCT 494
                                                                                                  CCAAGAGTGGAAGTGCGCTTTCATGGAGACCTCGGCCAAGATGAACTACAACGTCAAGGA 476
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Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Pa Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I (bases 1 to 709)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect mRNA sequence EST BG699614 BG699614 602679344F1 NIH_MGC_95 Homo sapiens human BG699614.1 GI:13968106 Homo 709 Palkovits, Michael J. sapiens þp mRNA cDNA clone linear Collection (MGC) IMAGE: 4811962 Euteleostomi; EST 07-MAY-2001 Homo

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Preparation:

M.D., Ph.D. Brownstein

(NHGRI),

Shiraki

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                           AA 539
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10703 row: h column: 11
High quality sequence stop: 701.
LOGATION/Qualifiers
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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79.5%;
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Pred. No. 7.9e-53;
0; Mismatches 103;
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Search completed: March 23, 2003, 17:12:31 Job time: 3887.38 secs

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                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
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597
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         March 23, 2003, 15:14:42; Search time 157.566 Seconds (without alignments) 2938.192 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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_	234.4	39.3	452	10	US-09-960-352-4253	Sequence 4253, Ap
2	204.6	34.3	454	10	US-09-960-352-5830	Sequence 5830, Ap
ω	151	25.3	3082	10	US-09-778-963A-1	Sequence 1, Appli
4	137.8	23.1	551	10	US-09-765-298A-25	25
υ	137.8	23.1	570	ဖ	US-09-359-595-7	Sequence 7, Appli
σ	137.8	23.1	570	10	US-09-765-298A-27	N
7	136.2	22.8	570	12	US-10-104-484-1	Sequence 1, Appli
œ	136.2	22.8	570	12	US-10-104-484-3	Sequence 3, Appli
9	118.2	19.8	3346	9	US-09-764-868-67	Sequence 67, Appl
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11	107.8	18.1	1119	9	US-10-067-813-1	Sequence 1, Appli
12	102.6	17.2	1085	9	US-10-067-813-3	Sequence 3, Appli
13	100.4	16.8	11221	10	US-09-778-963A-3	
14	99.	16.6	405	10	US-09-960-352-10273	Sequence 10273, A
15	97	16.2	368	10	US-09-864-761-21643	Sequence 21643, A
16	84.2	14.1	612	10	us-09-972-529-3	Sequence 3, Appli
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18	84.2	14.1	3192	10	US-09-788-654A-1	Sequence 1, Appli
19	81.2	13.6	3936	10	US-09-919-172-49	Sequence 49, Appl

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US-09-764-868-77	US-09-764-868-497	US-09-960-352-13143	US-09-925-302-91	US-09-822-849A-563	US-09-880-107-3029	US-09-764-868-507	US-09-962-832-224	US-10-108-605-44	US-09-764-868-69	US-09-764-868-84	US-10-098-841-237	US-10-044-090-111	US-09-917-800A-1704	US-09-801-368-285	US-09-917-800A-1389	US-09-817-182-1	US-09-817-198A-1	US-09-764-868-88	US-09-962-832-256	us-09-925-300-678	US-09-960-352-11732	US-09-801-368-287	US-09-967-736-4	US-10-044-090-110	US-09-764-868-501
Sequence 77, Appl	Sequence 497, App	Sequence 13143, A	Sequence 91, Appl	Sequence 563, App	Sequence 3029, Ap	Sequence 507, App	Sequence 224, App	Seguence 44, Appl	Sequence 69, Appl	Sequence 84, Appl	Sequence 237, App	Sequence 111, App	Sequence 1704, Ap	Sequence 285, App	Sequence 1389, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 88, Appl	Sequence 256, App	Sequence 678, App	Sequence 11732, A	Sequence 287, App	Sequence 4, Appli	Sequence 110, App	Sequence 501, App

## ALIGNMENTS

Db	Qy	Db	Qy	Db	Qy	Db	Qy	Ма	Qu	ûs-0			; SE(	 <u></u> 2	 Ω	٠. ٠ ٦ ٠	 a +a	; . A		 2 2	; GE	; Pai	. 80	RESULT	
181	214	121	154	61	94	1	34	Matches	Query Match	9-960-	DRGANI	TYPE: DNA	DID	JRRENI	JRRENT	ILE RE	TITLE OF	APPLICANT:	APPLICANT:	APPLICANT:	NERAL	tent N	-096-F	1	
CAGCGCCTTGCCATGCCAGGGGTCACGCCTTCATCCTGGTTTATTCTATCACCAGGAAG 240	CAGCGCCTGTCCATCTCCAAGGGCCACGCCTTCATCCTGGTGTTCTCCCGTCACCAGCAAG 273	CACAAGGCGGGTGCGCTGCACATCACCGACACCGCGGTGGCCGCCGCTACCGGGGCCTG 180	AAGAGCGTGTGCACGCTGCAGATCACAGACACCACCAGCCAG	TTCCGTGAGGCGTACCTGCCGACCATCGAAGATACCTACC	TTCCGCGACACCTACATCCCCCACCATCGAGGACACCTACCGGCAGGTGATCAGCTGCGAC 153	GTGATCGGCTCGGCCGTGGGCAAGAGCGCTCTGGTGCAAAGGTGGGTG	GTGTTCGGGGCGGCGGCGTGGGCAAGAGCTCGCTGGTGCTGCTGCTGCTGTGAAGGGCACG 93	0	ol Girilarit. 39.3%; Score 234.4; DB 10; Length 452;	) OTHER INFORMATION: CIONE ID: IN-LIB34-UNG-QI-EI-E3 US-09-960-352-4253	Bos taurus	LENGTH: 452	SEQ ID NO 4253	OF SEO ID NOS: 15113	CURRENT APPLICATION NUMBER: US/09/960,352	FILE REFERENCE: 16511.006/37-21(10298)C	OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND	I: Mathialagan, Nagappan	NT: Byatt, John C.	5	GENERAL INFORMATION:	Patent No. US20020137139A1	. Spointne AUSA Applipation [IS/09960352		

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Best Local S
Matches 277
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Wathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5830
LENGTH: 454
TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5830, Application US/09960352 Patent No. US20020137139A1
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                                                           CGTGCAGATCAAGGG---CAGCGTGGAGGACATCCCCGTGATGCTCGTGGGCAACAAGTG
                                                                                                                    GGTGTTCTCCGTCACCAGCAAGCAGTCGCTGGAGGAGCTGGGGCCCATCTACAAGCTCAT
                                                                                                                                                                TGGCCGNCGCTACCGGGGCCTGCAGCGCCTTGCCATTGCCAGGGTCACGCCTTCATCCT
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                                                                                                      GGTTTATTCTATCACCAGGAAGCAAACCCTGGAGGAGCTGAAGCCGCTCTTTGAGCTGAT
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72.5%;
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Pred. No. 8.5e
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8.5e-37;
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GENERAL INFORMATION:

APPLICANT: NEELAM, Beena et al
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001112
CURRENT APPLICATION NUMBER: US/09/778,963A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 5
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 3082
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; ORGANISM: Homo s
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Best Local Similarity
Matches 356; Conserv
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TGCATGCGC
                                  TGCACCCTC
                                                                    CCCGCCCTGCATCGCAAGATCTCCGTGCAGTACGGTGACGCCTTCCACCCCAGGCCCTTC
                                                                                                   CTCAACATCGACGGCAAGCGCTCCGGGAAGCAGAAGAGGACAGACCGCGTCAAGGGCAAA
                                                                                                                                       AACGTGGACGAGATGTTCTACGTGCTCTTCAGCATGGCCAAGCTGCCACACGAGATGAGC
                                                                                                                                                                                                            CTGCTGGTGTCGGGCGACGAGAACTCCGCCTACTTCGAGGTGTCGGCCAAGAAGAACACC
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Pred. No. 8.8e-25;
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                                                                                                                                                                       Sequence 7, Application US/09359595
Publication No. US20030003449A1
GENERAL INFORMATION:
APPLICANT: Menzel, R.
APPLICANT: Khazak, V.
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APPLICANT: ARONHEIM, AMI
APPLICANT: ARONHEIM, AMI
TITLE OF INVENTION: METHOD FOR DETECTION PROTEIN-PROTEIN INTERACTIONS AND A KIT
FILE REFERENCE: 108387.01
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Best Local
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETERMINATION OF TITLE OF INVENTION: PROTEIN FUNCTION AND IDENTIFICATION OF MODULATORS TITLE OF INVENTION: THEREOF FILE REFERENCE: 9366-005 CURRENT APPLICATION NUMBER: US/09/359,595 CURRENT FILING DATE: 1999-07-23 EARLIER APPLICATION NUMBER: 60/093,855 EARLIER FILING DATE: 1998-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/765,298A
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: IL 125456
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
NUMBER: OF SEQ ID NOS: 31
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ORGANISM: Homo sapiens
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RESULT 6
US-09-765-298A-27
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US-09-359-595-7
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                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 570
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Best Local Similarity 57.0%;
Matches 272; Conservative
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Best Local Similarity Matches 272; Conserv
                                  Query Match
                                                                                                                                                                                                 APPLICANT: ARONHEIM, AMI
TITLE OF INVENTION: METHOD FOR DETECTION PROTEIN-PROTEIN INTERACTIONS AND A KIT TH
FILE REFERENCE: 108387.01
CURRENT APPLICATION NUMBER: US/09/765,298A
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: IL 125456
PRIOR APPLICATION NUMBER: IL 128017
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1999-01-12
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SOFTWARE: PatentIn Ver. :
                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 31
                                                                                          TYPE: DNA
ORGANISM: Homo
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Pred. No. 5.6e-22;
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                                    DB 10;
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SEQ ID NO 1
LENGTH: 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stewart, Scott
TITLE OF INVENTION: METHOD OF INHIBITING CANCEROUS
TITLE OF INVENTION: GDP-BOUND CONFORMATION
FILE REFERENCE: UNICH-0010
CURRENT APPLICATION NUMBER: US/10/104,484
CURRENT FILING DATE: 2002-03-25
DBIOR APPLICATION NUMBER: 6/03-25
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/277,959
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Guan, Kun-Lian APPLICANT: Stewart, Scot
                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Nucleotide sequence of the GDP-bound Ras mutant,
                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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CAGGTGGTCATTGATGGGGAGACGTGCCTGTTGGACATCCTGGATACCGCCGGCCAGGAG
                                                                                                                                GAATATAAGCTGGTGGTGGTGGGCGCCGGCGGTGTGGGCAAGAATGCGCTGACCATCCAG 66
                                                                  CTGATCCAGAACCATTTTGTGGACGAATACGACCCCACTATAGAGGATTCCTACCGGAAG
                                                                                               TTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATCGAGGACACCTACCGGCAG 138
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 570
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APPLICANT: Stewart, Scott
TITLE OF INVENTION: METHOD OF INHIBITING CANCEROUS CELL PROLIFERATION USING
TITLE OF INVENTION: GDP-BOUND CONFORMATION
FILE REFERENCE: UMICH-0010
CURRENT APPLICATION NUMBER: US/10/104,484
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 60/277,959
PRIOR APPLICATION NUMBER: 60/277,959
PRIOR FILING DATE: 2001-03-23
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                                                                    GCCATCAACAACACCAAGTCTTTTGAGGACATCCACCAGTACAGGGAGCAGATCAAACGG
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                                                                                                                                                                          CAGTTCCCGGCCATGCAGCGCCTGTCCATCTCCAAGGGCCACGCCTTCATCCTGGTGTTC 258
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Pred. No. 1.3e-21;
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Best Local
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE
LOCATION: (2787)
OTHER INFORMATION: n e
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LOCATION: (2795)
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                                                                                                                                                                    CATCGTGCAGATCAAGGGCAGCGTGGAGGACATCCCCGTGATGCTCGTGGGCAACAAGTG
                                                                                                                                                                                                                                                      AGGAACTGAGCAGTTTGCCTCCATGAGAGATCTCTACATCAAAAACGGCCCAAGGTTTCAT
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 GCTGCTGACGC 499
                           CTGTCCTTTCATGGAGACATCGGCAAAAAGTAAATCAATGGTGGATGAACTTTTTGCTGA
                                                    GTGCGCTTTCATGGAGACCTCGGCCAAGATGAACTACAACGTCAAGGAGCTCTTCCAGGA 488
                                                                                                CGATGAGACGCAGCGGAGGCTGGACACGCGCGGAGGCGCGGTGGCCCAAGAGTGGAA 428
                                                                                                                                                                                                CCTGGTTTATAGCCTGGTTAATCAACAGTCTTTTCAGGATATCAAGCCAATGAGAGATCA
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                                                                                   TCTGGAACCAGAAAGAGAGGTTATGTCTTCAGAAGGCAGAGCTCTGGCTCAAGAATGGGG
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Pred. No. 1.6e-17;
0; Mismatches 233;
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; OTHER INFORMATION: n
US-09-764-868-490
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Best Local Similarity
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LENGTH: 688
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OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (610)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic
FILE REFERENCE: PTZ32
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LOCATION: (669)
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GATCGTCANGC
                                    GCTGCTGACGC 499
                                                                             CTGTCCTTTNATGGAGACATCGGCAAAAAGTAAATCAATGGTGGATGAACTTTTTGCTGA
                                                                                                                     GTGCGCTTTCATGGAGACCTCGGCCAAGATGAACTACAACGTCAAGGAGCTCTTCCAGGA 488
                                                                                                                                                              TCTGGAACCAGAAAGAGAGGTTATGTCTTCAGAAGGCANAGCTCTGGCTCAAGAATGGGG
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                                                                                                                                                                                                                                                                                                                               CCTGGTTTATAGCCTGGTTAATCAACAGTCTTTTCAGGATATCAAGCCAATGAGAGATCA
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52.1%;
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Pred. No. 1.4e-17;
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           Sequence 3, Application US/10067813
Patent No. US/20020156013A1
GENERAL INFORMATION:
APPLICANT: Renauld, Jean-Christophe
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Best Local (
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APPLICANT: Levitt, Roy
APPLICANT: Nicolaides, Nicholas
TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
TITLE OF INVENTION: Atopic Allergies and Related Disorders
FILE REFERENCE: 036870-5071
CURRENT APPLICATION NUMBER: US/10/067,813
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/157,247
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 17
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   APPLICANT:
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LOCATION: (19
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mes 243; Conserv
                                                                                                                                                                                                                                                               AGGTGGACACGCGCGAGGCGCAGGCGGTGGCCCAAGAGTGGAAGTGCGCTTTCATGGAGA 445
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Louahed,
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Louahed, Jamila
Grasso, Luigi
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Pred. No. 2.8e-15;
0; Mismatches 182
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-963A-3
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; NAME/KEY: CDS
; LOCATION: (102)..(725)
US-10-067-813-3
                                                                                                                                                                                                     Sequence 3, Application US/09778963A
Patent NO. US20020115172A1
GENERAL INFORMATION:
APPLICANT: NEELAM, Beena et al
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001112
                                                                                              SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Grasso, Luigi
APPLICANT: Levitt, Roy
APPLICANT: Nicolaides, Nicholas
TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
TITLE OF INVENTION: Asthma Associated Factors and Related Disorders
FILE REFERENCE: 036870-5071
CURRENT APPLICATION NUMBER: U$/10/67,813
CUGRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/157,247
PRIOR TILING DATE: EARLIER FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                             CURRENT APPLICATION NUMBER: US/09/778,963A CURRENT FILING DATE: 2001-02-08 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local
                                                                    LENGTH:
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 TACCGCGTGGTGGTCTTCGGGGCGGCGGCGCGTGGCCAAGAGCTCGCTGGTGCTGCGCTTC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCACTGACAAGGCCAGCTTTGAGCACGTGGACCGCTTCCACCAGCTTATCCTGCGCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCACCAGCAAGCAGTCGCTGGAGGAGCTGGGGGCCCATCTACAAGCTCATCGTGCAGATC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCCGGCCATGCAGCGCCTGTCCATCTCCAAGGGCCACGCCTTCATCCTGGTGTTCTCC 261
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56.2%;
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Pred. No. 3.9e-14;
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RESULT 14
US-09-960-352-10273
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APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/980,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10273
EENCTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10273, Appl Patent No. US2002013 GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (3),(23),(31)
OTHER INFORMATION: Clone ID: 44-LIB3058-050-Q1-K1-C8
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                       CGCTTCGTGAAGGGCACGTTCCGCGACACCTACATCCCCACCATCGAGGACACCTACCGG 135
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                                                                                       CAGGTGATCAGCTGCGACAAGAGCGTGTGCACGCTGCAGATCACAGACACCACCGGCAGC
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CGCGCATTCCCCGCCATGCGACGCCTCTGCATCCTTACCGGAGACGTGTTCATCCTAGGG
                            CACCAGTTCCCGGCCATGCAGCGCCTGTCCATCTCCAAGGGCCCACGCCTTCATCCTGGTG
                                                            AAGTTCTACTGCATTCGAGGCGAGAGGTACCAGCTGGACATCCTCGACACGTACGGCAAC
                                                                                                                        CGCTTCCTGACGGGCCGCTACGAGGACGCCTACACGCCCACCATCGAAGACTTCCACCGC
                                                                                                                                                                                     AACTGCTACCGCATGGTGGTCCTCGGCTCGTCCAAGGTGGGCAAGACGGCCATCGTGTCG
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                                                                                                                                                                                                                                                                  Similarity
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62.2%;
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Pred. No. 2.1e-13;
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US-09-864-761-21643
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SEQ ID NO 21643
LENGTH: 368
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001 V. FOR APPLICATION NUMBER: PCT/US01/00665 PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: DCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR ETLIANS CONTROL OF THE PRIOR APPLICATION NUMBER: US 09/508,400 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: US 09/774,203
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Penn, Sharron APPLICANT: Rank, David F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
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IN HELA, SIGNAL = 2.6
IN PLACENTA, SIGNAL = 2.6
IN PLACENTA, SIGNAL = 3
IN HELLOO, SIGNAL = 3
IN FETAL LIVER, SIGNAL = 3
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                                                                                                                                                                                                     Query Match 16.2%; Score 97; DB 10; Length 368; Best Local Similarity 65.4%; Pred. No. 5.7e-13; Matches 142; Conservative 0; Mismatches 75; Indels
                                               136 CAGGTGATCAGCTGCGACAAGAGCGTGTGCACGCTGCAGATCACAGACACCACCGGCAGC 195
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SUMMARIES

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## ALIGNMENTS

RESULT 1
AB076888/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS REFERENCE AUTHORS TITLE ORGANISM Kontani, K., Tada, M., Ogawa, T., Okai, T. and Katada, T. Di-Ras: A Distinct Subgroup of Ras-family GTPases with Unique Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens adult brain cDNA to mRNA, clone_lib:lambda ZAPII human brain cDNA. Homo sapiens mRNA for Di-Ras1, AB076888 AB076888.1 GI:21624247 AB076888 774 bp p mRNA l complete cds. linear PRI 25-JUN-2002

SOURCE

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Mammalia; Eutheria;
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AX430295
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                                                                                                                                                                                                                                                                                                                                                                        Chalup, M.S., Altus, C.M., Lincoln, S.E., Dufour, G.E. and Jackson, S.
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                                                                                                                                                                                                                                                                                                   INCYTE GENOMICS INC (US)
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/translation="MPEOSNDYRV"
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436 c
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                                                                                                               AX430418
Sequence
AX430418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@fri.co.) p, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center tec.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sujiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:OCBBF2
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Isogai, T. and Yamamoto, J.
Direct Submission
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/note="cloning vector:
750 c 983 g
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/db_xref="taxon:9606"
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                Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens, similar to Rig protein, clone MGC:33391 mAGE:4814337, mRNA, complete cds
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                                                                                                                                                                                                                                                                                                                                                                                                          Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                   prediction
                                                                                                                                                                                                                                                                                                                                        contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Michael J. Brownstein (NHGRI) &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                               http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
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/db_xref="taxon:9606"
/note="Incyte ID No: LI:332161.1:2000SEP08"
1 840 c 927 g 688 t
                                                                  /organism="Homo sapiens"
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
                                   /note="Vector:
                                                       /lab_host="DH10B"
                                                                                                                                                                                Location/Qualifiers
1. .3391
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lamerdin, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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9 CTCACATGAGGGTGCATTTGCCC 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-FEB 1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere. BC41195 (CIT-B-31c16) is currently separated from cosmid R32203 (AC006275) to the left by a sequence gap of approximately 6 kb, and overlaps BAC 103889 (CIT-B-191n6; AC006130) to the right from bases 175,545 to 177,540. Additional map and sequence information are available at: http://www-bio.llnl.gov/bbrp/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Sanders, C., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC006538 177540 bp DNA linear PRI 07-FEI Homo sapiens chromosome 19, BAC 41195 (CIT-B-31c16), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   serine protease gene cluster Unpublished
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1 (bases 1 to 177540)
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FQELLTLETRRNNSLNIDGKRSGKQKRTDRVKGKCTLM"
3 996 c 1016 g 729 t
                                                                                                                                                                                                                                                               /clone="CIT-B-31c16"
/clone=lib="Cal tech CIT-B BAC library"
/note="LLNL clone name: BC41195"
complement(1. .144)
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                                                                   complement(868.
                                                                                                                      complement(438.
                                                         /rpt_family="AluSx"
complement/per
                                                                                                                                                                                complement(399.
/rpt_family="L1MB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="similar to Rig protein"
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2.3;
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repeat_region	repeat	repea	repea	repe	repea	repea	repea	repea	repea	repeat	repeat	repeat	repeat.	repeat.	mis	rep	rep	rep	repe	repe	repe	rep	repe	repeat	reneat.	repeat.	repeat_	repeat_	repe	repe	repe	repea	repe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Camppiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacConald, P., Major, J., Marquis, N., Meneus, L., Mihova, T., Menaya, V., Murphy, T., Naylor, J., Weneus, L., Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Collara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Severy, P., Spencer, B., Stange-Thoman, N., Stongeback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thoman, J., Tosfave, S., Theodore, J., Strauss, N., Subramanian, A., Talamas, J., Tosfave, S., Theodore, J.
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N
                                                                                                                                   Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Ilicy, I.,
Johnson, R., Jones, C., Kamat, A., Karats, A., Kells, C., Lahocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
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                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Boukhgalter,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 Charles Street,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (01-MAR-2002) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consists of 14 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         provided by the submittor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence will be replaced
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Consensus quality: 189249 bases at least Q40
Consensus quality: 191283 bases at least Q30
Consensus quality: 192097 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L23814
Center clone name: 361_0_11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 7.8 in Q20 bases; Quality coverage: 7.9 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 194000; agarose-fp
Insert size: 193156; sum-of-contigs
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                                                                                                                                                                                      147951 148050: gap of 100 bp
148051 179165: contig of 31115 bp in length
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                                                                           Location/Qualifiers
/organism="Mus musculus"
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51238: contig of 16439 bp in
51338: gap of 100 bp
70476: contig of 19138 bp in
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14544: contig of 6851
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/db_xref="taxon:10090" /clone="RP23-361011"

/clone_lib="RPCI-23 Female Mouse BAC"

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                          DOE Joint Genome Institute.
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148051. .179165
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SOURCE
ORGANISM
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6 ATTCTCACATGAGGGTGCATTTGCCC 31
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                                                                                                                                                                                                                                                         Castro, A.F. and Quilliam, L.A. Identification of Rig, a nove with NOEY2 and Rap
                                                                                                                      Submitted (13-SEP-2001) Biochemistry and Molecular University School of Medicine, 635 Barnhill Drive,
                                                                                                                                                                                     3 (bases 1 to 597)
Castro, A.F. and Quilliam, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 597)

Ellis, C.A., Vos, M.D., Howell, H., Vallecorsa, T., Fults, D.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Mar 30, 2002 this sequence version replaced gi:18767414. Sequence Quality Assessment: This entry has been annotated with sequence quality
                                                                   Indianapolis, IN 46202, USA Location/Qualifiers
                                                                                                                    University School of Medicine,
                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                             Rig is a novel Ras-related protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This entry has been annotated with sequence quality
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
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of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality levels above 40 are expected 1 error in 10,000 bp.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .153873
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37090 c 39282 g
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/db_xref="taxon:9606"
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-OCT-2001) Dept. of Cardiology, U.T. MD. Anderson Cancer Center, 1515 Holcombe Blvd-449, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                      Similarity
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                                                                     Conservative
                                                                                                                                                      /product="small GTP-binding tumor suppressor 1"
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/protein_id="AAL17968.1"
/db_xref="G1:16508176"
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LIVQIKGSVEDIPVMLVGNKCDETQREVDTREAQANAQEWKCAFMETSAKMNYNVKEL
FQELLTLETRRMMSLNIDGKRSGKQKKTDKVKGKCTLM"

178 c 195 g 90 t
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/Product="Rig protein"
/Product="Rig protein"
/Product="GI:1655534"
/db_xref="GI:1655534"
/translation="MPPDSNDYRVVVFGAGGVGKSSLVLRFVKGTFRDTYIPTIEDTY
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LIVOIKGSVEDIPVMLVGNKCDETQREVDTREAQAVAQEWKCAFMETSAKMNYNVKEL
FQELLTLETRRNMSLNIDGKRSGKQKRTDRVKGKCTLM"
a 178 c 195 g 90 t
                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="derived from dbEST AI497811"
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                                                                                                                                                                                                                                                                                                                         /note="GBTS1"
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                                                                                                                                                                                                                                                                                                                                                               'chromosome="19"
                                                                                    71.0%;
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Primates;
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Pred. No.
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zalnoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-MAY-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------Project Information
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Center project name: L9990 Center clone name: 365_F_21
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REFERENCE

TITLE AUTHORS JOURNAL

AUTHORS

REFERENCE

SOURCE ORGANISM KEYWORDS VERSION ACCESSION DEFINITION

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COMMENT

NOTE: This record contains 80 individual

sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone

However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will

be preserved.

1629 1729 2484 ### 157: contig of 757 bp in length

### 857: gap of 100 bp

### 1628: contig of 771 bp in length

### 1728: gap of 100 bp

### 2483: contig of 772 bp

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5864: cr

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10192:

2659 12758: 810 11909:

30598 3134, 31348 31447: (

31347: contig of 447: gap of 32194: contig of

30597: 29742:

31347: cont

28878: 28029:

1878: gap of 29642: contig c 1742: gap of 30497: contig c

27183:

183: gap of 27929: contig c 029: gap of 28778: contig c

26327: 25478: 24617: 23760: 22908: 22059: 21209:

33147: 32294:

33047: contig 147: gap of 33879: contig

100 b of 732

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Earnhart, C., Edgar.D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Lieu, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Kovar, D., Louseged, H.,
Lozado, R., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Massey, E., Mawhiney, E., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morts, S.,
Myugen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rulz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, M., Tomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Williams, G., Williamson, A., Wleczyk, R., Woden, S., Worley, K.,
Williamson, M., Williamson, A., Wang, A.,
Williamson, M., Williamson, M., Willi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouck, J., Buhay, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329
Consensus quality: 131591 bases at least Q40
Consensus quality: 137671 bases at least Q30
Consensus quality: 141923 bases at least Q20
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Project Information
                                                                                                                                                                                                                                                                         Center project name: GQOS
Center clone name: CH230-96H21
                                                                                                                                                                                                         Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM
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Burch,P.,
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
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Trichocomaceae; to 3255)
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                                                                                                Published Only in Database (2002)
2 (bases 1 to 137615)
Sasaki,T., Matsumoto,T. and Katayose,Y.
                                                                                                                                                             Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DN clone:B1121A12
                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                   AP005284 137615 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 2 *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                     Direct Submission
Submitted (29-MAY-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA clone:B1121A12.
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                  Agrobiological Sciences, Rice Genome Res
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
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(E-mail:tsasaki@nias.affrc.go.jp,
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/protein_id="aak39062.1"
/db_xref="G1:13517939"
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READAIFYXKTSVPQTLMVCETVNNIIIGRTVNPRNKNWSCGGSSGGEAMIGFRGGVIG
VGTDIGGSIRVPAAFNFLYGLRPSHGRLPYAKKNSMEGQETVHSVVGPIAHSVGDLR
LFTTSVLAQEPWKFDSKVIPMFWRQAEADIIKSKISSGCLNLRFYNFDGNVLJHPPIL
RGIDLAVAALTKAGHTVSPWTPYKHGFAHDLINNIYAADGSADVMAAINASGEPAIPN
IKDLLNPDIKAISMNKLWDTNLEKWKYQMEYLEQWAQAEEEAGKEIDAIIAPITPTAA
VRHQFKYYGYASVINLLDWTSVVVPYTFAESKVDTKREYQPVSELDKAVQDEYDPEV
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                                        Rice Genome Research Program;
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  URL:http://rgp.dna.affrc.go.jp/
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   Bouck, J., Bouid, S., Brieva, M., Brown, E., Bryant, N., Boulli, D., Bouck, J., Bowid, S., Brieva, M., Brown, E., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chowdhy, I., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Eagar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Harris, K., Garner, T., Garza, N., Gill, R., Gablsi, A., Gaorela, A., Garner, T., Garza, N., Gill, R., Gablsi, A., Gavara, M., Gunaratne, P., Hale, S., Hamilton, K., Garrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Garzell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Jackson, L.E., Li, J., Li, K., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Landry, M., Mershiney, E., McLeod, M.P., Meador, M., Martinez, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Woyen, N., Woyen, R., Pave, A., Payton, B., Peerv, J., Perez, L..
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* NOTE: This is a 'working draft' sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C. Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Blankenburg,K., Bonnin,D., Barbaria,J., Benton,J., Biange,K., Blankenburg,K., Bonnin,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
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/cultivar="Nipponbare"
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baylor Plaza,
3 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length
(see http://www.lbgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 54 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 115979 bases at least Q40
Consensus quality: 120179 bases at least Q30
Consensus quality: 123722 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Qy 3 ( Db 4763 (	Query Match Best Local Similarity Matches 23; Conser													
GGAAT GGAAT	tch al Si 23;	*	*	*	*	*	*	*	*	*	*	*	*	*
3 GGAATTCTCACATGAGGGTGCATTTGC 29	al Similarity 85. 23; Conservative	146616	146516	140149	140049	132231	132131	127286	127186	121503	121403	117533	117433	112473
AGGGTGCA:	66.5%; 85.2%; ative	155083:	146615:	146515:	140148:	140048:	132230:	132130:	127285:	127185:	121502:	121402:	117532:	117432:
TTTGC 29	Score Pred. 0; Mis	contig	gap of	contig.	gap of	contig	gap of	contig	gap of		gap of	contig	gap of	contig
89	Score 20.6; DB 2; Length 155083; Pred. No. 52; 0; Mismatches 4; Indels 0;	contig of 8468 bp in length.	gap of unknown length	contig.of 6367	gap of unknown	of 7818	unknown	contig of 4845	unknown	of 5683	unknown	of 3870	unknown	of 4960
	DB 2;	bp in	length	bp in length	length	bp in length	length	bp in length	length	bp in length	length	bp in length	length	bp in length
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Search completed: March 23, 2003, 16:04:28 Job time: 339.909 secs

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Database
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N_Geneseq_101002:*

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4: /SIDS2/gcgdata/ge
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31
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT: *
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Listing first 45 summaries
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1936.775 Million cell updates/sec
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710 2484	433 527	21521 294	21521	3061	1249	Length DB	
22	22	22 24	22	24	24		
AAF58344 ABA20286	AAK52951 AAK51967	AAK78175 ABN20378	ABA21357	ABO72648	ABQ72525	ID	SOME
Human GTP-binding Human nervous syst	Human polynucleoti Human polynucleoti	Human immune/haema Human ORFX polynuc			Human MDDT encodin	Description	ES

i iii ii	AAK09711	S	77.	57	17 8	44		
Human foetal	ABA61413	22	514	57.4	٠	43		
EST C	AAV88071	20	296	57.4	17.8	42		
FRAP (	AAV28518	19	7943	58.1	18	41	o	
Human RAPT1 c	AAT33872	17	7824	58.1	18	40	o	
pUC19-Sep1-5	AAD22153	24	7653	58.1	18	39	o	
Human	AAQ60348	14	353	58.1	18			
Human	ABL33369	24	9817	58.7		37		
4 Human secreted pro	AAC59514	21	1809	58.7	٠	36		
	AAC32810	21	1325	58.7	٠	35	c	
	ABQ65887	24	661	58.7	•	34	ဂ	
Prostate ca	ABL69695	24	470	58.7	18.2	33		
9 Kidney cancer rela	ABL68479	24	470	. 58.7		32		
Kidney	ABL68241	24	470	58.7	٠	31		
Human benign p	ABK64694	24	470	58.7	18.2	30		
Gene #	ABN96653		470	58.7	•	29		
Novel human	AAF66850		335	58.7	18.2	28		
Murine NR6	AAD04198		11832	59.4	18.4	27	c	
	AAV27148		11832	59.4	•	26	c	
Murine haem	AAD04197		6663	59.4	•	25	O	
Nucleotide	AAV27145		6663	59.4	18.4	24	c	
Human	AAH14598		3912	59.4	18.4	23	ဂ	
Human	AAS15815		3910	59.4	18.4	22	۵	
Human drug	AAH76202		3844	59.4	18.4	21	a	
9 cDNA encoding huma	AAA23459		3098	59.4	18.4	20	o	
Human cDNA	AAS08646		2936	59.4	18.4	19	O	
Human cDNA	AAH18429		2824	59.4	18.4	18	o	
	AAZ17527	20	787			17		
	AAS46692	22	24259		18.6	16		
	ABK42245	23	12932	61.3	19	15	a	
1 Human benign pros	ABK64471	24	340	•		14		
	ABN95508	24	340			13		
	AAF89024	22	3098	62.6		12	c	
Nucleotide se	AAZ00362	20	3098	•	19.4	11	C	
7 Human nervous sys	ABA20287	22	2484	•	19.8	10	c	

## ALIGNMENTS

RESULT 1
ABQ72525/c
ID ABQ725
XX ABQ725
XX ABQ725
XX ABQ725
XX Human
XX ABQ725
XX ABQ725
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XX HOMO S
XX WO2002
XX YO6-SEP
PR 06-SEP
PR 06-SEP 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout; neuroprotective; antirheumatic; antiarthritic; gene; ss. 06-SEP-2000; 06-SEP-2001; WO200240715-A2 03-SEP-2002 ABQ72525; ABQ72525 standard; cDNA; 1249 23-MAY-2002 sapiens. MDDT encoding cDNA SEQ ID 2000US-230505P. 2000US-230514P. 2000US-230515P. 2000US-230517P. 2000US-230518P. 2000US-230519P. (first entry) 2001WO-US27628 ВP ö 77.

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                                                                                                                                                                        The invention relates to an isolated human disease detection and control of treatment (MDDT) polypeptide (I) selected from a polypeptide having a convenience selected from 254 sequences (ABP51231-ABP51484) given in the control of t
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Best Local
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06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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06-SEP-2000;
07-SEP-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
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                                                                                                           Sequence 1249
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                                                      Local
9
CTCACATGAGGGTGCATTTGCCC
                                                                                                                                                                hybridisation
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                                                    Similarity
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Bradley DL, Rohatgi SD, Harris B, Roseberry
Peralta CH, David MH, Panzer SR, Flores V, D
Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                           BP;
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                                                                     Score
                                                        Pred.
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                                   Mismatches
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                                                                                                         0 other;
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                                                                     Length 1249;
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                                   Indels
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RESULT 2
ABQ72648/c
06-SEP-2000;
07-SEP-2000;
07-SEP-2000;
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06-SEP-2000;
06-SEP-2000;
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06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allergy; multiple scleros rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antianflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigo neuroprotective; antirheumatic; antiarthritic; gene; ss.
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06-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDDT; disease detection and treatment molecule polynucleotide;
                                                                                                                                                                                                                                        INCYTE GENOMICS INC.
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2000US-230517P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sclerosis;
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Daffo A;

e.g.

Hillman AM; Dahl CR;

JL;

WPI; 2002-527544/56. P-PSDB; ABP51431. мотіуата мG, Jones AL, R, s, Lincoln SE, Altus CM, Dufour GE, Chalup ms, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Yu TY, Wright RJ, Roseberr R, Plores V, Chen ΑJ, DL, RONAEGI DE, RONAEGI SR, F CH, David MH, Panzer SR, F Chang SC, Au AP, Inman RR; Chalup MS, H TF, Yap PE, B, Roseberry Hillman Dahl AM; A; CR;

e.g. Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder

Claim Page 414; 618pp; English.

The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51231-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds (I) or modulates the activity of (I), and for preparing a polycional or monoclonal antibody by hybridoma technology. Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for expression of a target for

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ID ABA21357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc detecting MDDT in a sample or for assessing toxicity of a test compound, ci in a diagnostic test for a condition or a disease associated with the cexpression of MDDT in a biological sample, for detecting (I) in a sample, cand for purifying (I) from a sample. For detecting (I) in a sample, cand for purifying (I) from a sample. A composition comprising (I), an associated with decreased or increased expression of functional MDDT. (C (I) or (II) are useful for diagnosing, treating or preventing disorders associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, carbonish, hepatitits, psoriasis, and cancer and an autoimmune/inflammatory disorder such as AIDS, Addison's disease, callergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or rheumatoid arthritis. (II) are useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 23
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hapatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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Similarity 100.0%;
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2000US-0179065.
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2000US-02174864.
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2000US-0218290
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2000US-0231497
2000US-0231497
2000US-02314186
2000US-0241186
2000US-0241186
2000US-02441806
2000US-02441806
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(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
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                                                                                                                                                                                                                                                                                                       Nucleic acids encoding useful for preventing, cancers and metastases
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diagnosing
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                                                                                                                                                                                                                                                                                                                        nervous system antigen polypeptides, and/or treating nervous system
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colitis;

multiple sclerosis,
(c) cardiovascular

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RESULT 4
AAK78175,
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18 - APR - 2000
19 - MAY 2000
07 - JUN - 2000
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17-MAR-2000;
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                  2000US-0225266
2000US-0225267
2000US-0225268
2000US-0225270
2000US-0225447
2000US-0225757
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2000US-0226681
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2000US-0220963.
2000US-0220964.
2000US-0224518.
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2000US-0225213.
2000US-0225214.
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2000US-0215135.
2000US-0216647.
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2000US-0190076
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                                                                                                                                                                                                                                                                                                                                                                                                                                      haematopoietic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO:32987.
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RESULT 5
ABN20378/c
                                                                                                                                                                     Qy
                                                         B
                                                                                                                                                                                          CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) CC amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (1) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (1) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (1) by expressing inactive proteins or to CC supplement the patients own production of (1). Additionally, (1) CC polynucleotides may be used to produce the secreted (1), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (1) proteins and polynucleotides may be used to prevent, CC cancers and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic acitigen genomic concerns the present human immune/haematopoietic antigen genomic concerns the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                               Query Match
Best Local S
Matches 23
                                                         16126 GCGGAATTTCCACATGAGGAAGCAGTTG 16099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acionseful for pretastasis
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01-DEC-2000
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08-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
17
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NOV-2000;
                                                                                  Н
                                                                        GCGGAATTCTCACATGAGGGTGCATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-483426/52.
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acids encoding human immune/hematopoletic antigen polypeptides, for preventing, diagnosing and/or treating cancers and is -
                                                                                                                                                                     21521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-02449216
2000US-0249216
2000US-0249216
2000US-0249218
2000US-0249218
2000US-0249244
2000US-0249264
2000US-0249264
2000US-0249264
2000US-0249297
2000US-0249297
2000US-0249390
2000US-025160
2000US-0251930
2000US-0251930
2000US-0251133
2000US-0251133
2000US-0251133
2000US-02511479
2000US-02511479
2000US-02511856
2000US-02511856
2000US-02511856
2000US-02511858
                                                                                                                Conservative
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2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENOME SCI INC
                                                                                                                                                                     BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO
                                                                                                                                                                     6512 A; 4334 C; 4422
                                                                                                                            64.5%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          32987; 3071pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben
                                                                                                             Score 20; DB
Pred. No. 30;
0; Mismatches
                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM;
                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Listing; English
                                                                                                                                                                     <u>ი</u>
                                                                                                                                                                     6253 T; 0 other;
                                                                                                                                         22;
                                                                                                                                         Length 21521;
                                                                                                                Indels
                                                                                                               0,
                                                                                                               Gaps
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2000US-0227009
2000US-0229344
2000US-0229345
2000US-0229345
2000US-0229345
2000US-0229345
2000US-0229345
2000US-0229345
2000US-0231243
2000US-02311243
2000US-02311413
2000US-02311413
2000US-02311413
2000US-0231160
2000US-023160
2000US-02316

02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000;

27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 21-SEP-2000; 25-SEP-2000;

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000;

14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

14-SEP-2000;

08-SEP-2000; 08-SEP-2000; 12-SEP-2000;

08-SEP-2000; 08-SEP-2000;

06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

13-OCT-2000 13-OCT-2000 20-OCT-2000 20-OC

0;

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CC (referred to as open reading frame, ORFX, where X is 1-1149] (see Table 1 cin the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated cd disorder in humans, and in the manufacture of a medicament for treating a CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, corporatesis, benign tumours, keloid, degenerative disorders related to organ contensis, hearign tumours, keloid, degenerative disorders related to organ contensis, hearign tumours and the disorders, disorders follets, systemic contensish benign tumours desease, diabetes mellitus, systemic contensish hyperthematosus, hypertension, hypothyroidism, cholesterol ester contension autoimmune deficiencies and disorders, infectious contensish autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also conseill for treating burns, incisions, ulcers, for treating osteoporosis,
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degenerative disorder; psoriasis; benign tumour; haemorrhage; cardiovascular disease; diabetes mellitus; systemic lugus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; hymnune deficiency; immune disorder; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                          bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID 9233; 1037pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-106308/14.
P-PSDB; ABP04626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myasthenia gravis; gene; ss.
                                                      Sequence
                                                                                                                                          systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000;
29-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX polynucleotide sequence SEQ ID NO:9233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-2002
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                                                                                                          pecification,

    The sequence data for this patent did not form
scification, but was obtained in electronic format
ftp.wipo.int/pub/published_pct_sequences.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes substantially purified human proteins
                                                      294
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                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-206132P
2000US-228716P
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                                                      59
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                                                      Α.
63.98;
                                                      83 C;
                  Score 19.8;
                                                      84 G;
                                                      67
                                                      T; 1 other
                  DΒ
                  24;
                Length
                                                                                                      part of the printed directly from WIPO
                                                                                                                                                          resulting from
                  294;
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Matches

Similarity

Conservative

0

Mismatches

7;

Indels

0

Gaps

0

Pred. No.

16;

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RESULT 6
AAK52951/
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                                 Query Match
Best Local
                       Matches
                                                                                                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating
                                                                                                                                                                                                                                                                                                                                                                      Tang
Zhao
                                                                                                                                                                                                                                                                 Claim 1; Page 4758-4759; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                    Sequence
                                                                                         (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                 activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                      useful in diagnosis and
                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like activities
                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                            Xue
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK52951 standard; cDNA; 433
                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine;
                                                                                                                Note: Records for SEQ ID NO 2110 (AAK52581),
                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000;
                                                                                                                             inflammation.
                                                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CTCACATGAGGGTGCATTTGCCC
                                                                                                                                                                                                                                                                                                                                                       , VT,
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DB; AAM79818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                      21;
                                                                                                                                                                                                                                                                                                                                                                                                        HYSEQ INC.
                                  Similarity
                                                                     433
                                                                                                                                                                                                                                                                                                                                                         Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0496914
2000US-0560875
2000US-0598075
2000US-0620325
2000US-0654936
2000US-0663561
2000US-0693325
                       Conservative
                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US04098
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                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0728422
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                                                                    90 A; 145 C; 113 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                         Wang J, Z
Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT,
Wang J, Zl
                                 63.9%;
                                                                                                                                                                                                                                                                                       gene
                      0;
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E, Goodrich
                                 Score 19.8;
Pred. No. 17
                                                                                                                                                                                                                                                                                       therapy
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                       Mismatches
                                                                    84 T; 1
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                                                                                                                                                                                                                                                                                                                                                                        Ren
                                                                                                                                                                                                                                                                                                                                                            7,
                                             DB
                                                                                                                                                                                                                                                                                                                                                                     Zhou
F, c
                                                                                                     2111
from
                                             22;
                                                                    other;
                       <u>ب</u>
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                                             Length
                       Indels
                                                                                                     the sequence listing
                                                                                                                 (AAK52582)
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R, Wang
                                              433;
                                                                                                                                                                                                                                                                                                                                                                                 Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy;
                       0
                                                                                                                and 3666
                       Gaps
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                       0
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В

348

CTCACAGGATGGTGCATTTGCCC

326

Вb

347

CTCACAGGATGGTGCATTTGCCC

325

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RESULT 7
AAK51967/c
ID AAK51967
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                                              Query Match
Best Local
                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                                                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemmia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                           Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                  Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haematop tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                 Claim 1; Page 1850-1851; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157190-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK51967;
                                                                                                    Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                         useful in
                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like
                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                 Sequence
                                                                                                                                         inflammation.
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20-OCT-2000;
              9
                                                                                                                                                                                                                                                                                                                                          2001-476283/51.
DB; AAM78834.
             CTCACATGAGGGTGCATTTGCCC
polynucleotide
                                    Similarity
21; Conser
                                                                                                                                                                                                                                                                                                                                                                           , Wang D,
Yang Y,
                                                                                 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                  Liu
                                                                                                                                                                                                                                                                                                       diagnosis and gene
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2000US-0560875.

2000US-0598075.

2000US-0620325.

2000US-062936.

2000US-0654936.

2000US-0693325.

2000US-0693325.

2000US-0728422.
                                    Conservative
                                                                                BP;
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                                                                                 111
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Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT, Asundi V,
Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID
                                              63.9%;
                                                                                A; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527
                                    0
                                                                                C; 129
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                                                       Score 19.8;
                                  Pred. No. 18;
); Mismatches
                                                                                                                                                                                                                                                                                                        therapy
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F, c
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from
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                                                                                 0 other;
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Chen
                                   2;
                                                                                                                 (AAK52582) and 3666
the sequence listing
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Wang
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7 ZW;
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RESULT 9
ABA20286/c
ID ABA20286 standard; DNA; 2484 BI
XX
AC ABA20286;
XX
DT 23-JAN-2002 (first entry)
XX
DT 23-JAN-2002 system related po
                                                                                                                                  В
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                                                                                                                                                                                                                                 RESULT 8
AAF58344/c
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1999;
23-AUG-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                          The present invention relates to novel human guanosine triphosphate (GTP)-binding associated proteins (GBAPs; AAB66501-AAB6856) and their coding sequences (AAF58301-AAF5836). The proteins and coding sequences of the present invention are useful for treating a variety of disorders including inflammation, AIDS, Addison's disease, anaemia, arteriosclerosis, asthma, autoimmune disorders, Grave's disease,
                                                                                                                                                                                                                                                                                                                                                                                    New guanosine triphosphate-binding associated proteins (GBAP) encoding nucleic acids, useful for treating and/or diagnosing associated with GBAP expression, such as cancer, diabetes and
                                                                                                                                                                                                                              Sequence 710
                                                                                                                                                                                                                                                      hepatitis, multiple sclerosis, cancer, diabetes, psoriasis.
                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 216; 233pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; guanos inflammation;
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ч J,
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99US-0159849.
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RESULT 10
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                                                                                                                                                  Human; nootropic; neuroprotective; cytostatic; immunosuppressive; antiinflammatory; anti-HIV; antiparkinsonian; antisickling; antianaemic; ar
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ABA20287 standard; DNA; 2484
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                                                            sapiens.
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2000US-0251868.
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Pred. No. 24;
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                                                                                                                                                 c; dermatological; virucide;
V; antibacterial; vulnerary;
antiarthritic; cancer;
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2000US-0241809.
2000US-0241826.
2000US-0242221.
                                                                                                                                                                        2000US-0249297
2000US-0249299
                                                                                                                                                                                                                                                                                                                                                                                                2000US-0246523
2000US-0246524
                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0246474.
2000US-0246475.
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2000US-0241787.
                                       GENOME
                       sc,
                                       SCI INC
                       SM:
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AAZ00362/c
ID AAZ00362 standard; DNA; 3098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 21
                                                                                                                          14-JAN-1999;
15-JAN-1998;
20-JUL-1998;
04-DEC-1998;
14-JAN-1999;
14-JAN-1999;
14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antipagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital:
                                                                                                                                                                                                                                                                                                                                                           Fatty
fatty
          WPI; 1999-444398,
P-PSDB; AAY14952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2036 CTCACAGGATGGTGCATTTGCCC 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2484 BP; 440 A; 906 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                       Gimeno
                                                                                  (MILL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                               14-JAN-1999;
                                                                                                                                                                                                                                                                          22-JUL-1999
                                                                                                                                                                                                                                                                                                     WO9936537-A2
                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ00362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 12618; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 CTCACATGAGGGTGCATTTGCCC 31
                          1999-444398/37
                                                                                                                                                                                                                                                                                                                                                           acid transport protein; FATP; long chain fatty acid; LCFA; acid; FATP biosynthesis; obesity; diabetes; heart disease;
                                                       RE,
                                                                                  MILLENNIUM PHARM INC
WHITEHEAD INST BIOME!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     sequence of rat rnFATP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastases
                                                       Hirsch DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                          990S-0232201.
980S-0091491.
980S-0093491.
980S-0110941.
990S-0232195.
990S-0232197.
990S-0232200.
                                                                                                                                                                                                                                               99WO-US00182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.9%;
91.3%;
                                                                                   BIOMEDICAL RES
                                                        Lodish HF,
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Pred.
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                                                        Stahl
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                                                        Tartaglia LA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rebral anoxia and bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2484;
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ARESULT 12
AAF890
XX AAF890
XX AAF890
XX AAF890
XX AAF890
XX Fatty
XW Fatty
KW Yeast;
KW Weight
XX WO2001
XX WO21-SEP
PR 23-SEP
PR 17-FEB
PR 17-FEB
PR 16-DEC
PR 17-FEB
PR 18-DEC
PR 17-FEB
PR 18-DEC
PR 18-DE
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                           23-SEP-1999;
23-SEP-1999;
16-DEC-1999;
17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding the proteins are provided. The FATP proteins can be produced by standard recombinant methodology. Fatty acid uptake by cells can be modulated by modulated by modulating biosynthesis of FATP proteins especially FATP6. In particular, antisense oligonucleotides can be used to modulate FATP biosynthesis. Modulation of FATP6 is useful for inhibiting fatty acid uptake in cardiac muscle of humans. Agents can be directed to cardiac muscle or liver by administration of a complex of the agent and a FATP6 binding moiety. DNA encoding FATP proteins can be used as a reference used in detecting variant alleles or homologues. Altering the LCFA uptake by administering an inhibitor or enhancer of FATP transport function in the small intestine can decrease or increase calories available as fats, and can decrease or increase circulating fatty acids. Blocking the function of FATP4 and also FATP2, is useful for treating obesity,
                                                                                                                                                                                                                                    (WILL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2433 CTGACATGAGGGTGCATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides a family of fatty acid transport proteins (FATPs) that mediate transport of long chain fatty acids (LCFAs) across cell membranes into cells. Human and murine FATP proteins and nucleic acids
                        New fatty acid transport proteins (FATPs) useful for the manufacture medicament for treating obesity, diabetes and heart disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000; 2000WO-US25891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200121795-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat FATP1 coding sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF89024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF89024 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fatty acid transport proteins and related polynucleotides, useful for treating obesity, diabetes and heart disease
                                                                                                                                                                                                                                                                                                                      06-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3098 BP; 614 A; 911 C;
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                                                                                                                               2001-354783/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid transport protein; FATP; human; mouse; rat; rice blast
; fat absorption; obesity; diabetes; heart disease; hyperlip;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                          AAB83252
                                                                                                                                                                                                                                       WHITEHEAD I
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                                                                                                                                                                                   Hirsch DJ,
                                                                                                                                                                                                                                                                                                                99US-0405504.
99US-0405505.
99US-0465280.
2000US-0506252.
2000US-06111197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis;
                                                                                                                                                                                                                                       INST BIOMEDICAL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.6%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  obesity; diaperes, ....
colosis; TB; anti-fungal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                      HF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              903 G; 670 T;
                                                                                                                                                                                                                                                                  RES
                                                                                                                                                                                      Gimeno
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                                                                                                                                                                                   RE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                   Tartaglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ice blast fungus;
hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                      of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic

carcinoma in a patient.

The method is

useful

identifying

progression of liver cancer, hepatocellular carcinoma or metastatic tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level

The invention relates to a novel method for diagnosing

and

detecting the

from of

Claim

1; SEQ ID NO 2006; 298pp; English

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes liver tissue sample

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WPI;

2002-426119/45

(GENE-) 02-OCT-2000;

GENE LOGIC INC.

2000US-237054P

Ď,

Alvares C,

Peres-Da-Silva

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Vockley

02-OCT-2001; 2001WO-US30589.

11-APR-2002.

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RESULT 13
ABN95508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of fatty acid transport proteins (FATPS) from a number of species, including FATP1, FATP2, FATP3, FATP4, FATP5 and FATP6 from the human, FATP1-FATP5 from the mouse, FATPa and b from C. elegans, and FATP from Aspergillus nidulans, Drosophila, zebrafish, Magnaporthe grisea, Mycobacterium tuberculosis and Cochliobolus heterostrophus. The FATP from M. tuberculosis can be used to identify inhibitors which can then be used to treat TB. That from M. grisea (also known as rice blast fungus) can be used to develop anti-fungal agents capable of preventing infection of rice. Those from the human can be used to develop treatments for diabetes, heart disease, obesity, hyperlipidaemia and weight control. The present sequence is one of the sequences described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                          Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene #2006 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN95508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                               WO200229103-A2
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN95508 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCACATGAGGGTGCATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGACATGAGGGTGCATTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3098 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; 287pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     614 A; 911 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.6%;
95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     903 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     670 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DΒ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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RESULT 14
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        The invention relates to a method of diagnosing (I) the onset or C progression of benign prostatic hyperplasia (BPH), or screening (II) for C progression of benign prostatic hyperplasia (BPH), or screening (II) for C ridentifying an agent that modulates the onset or progression of BPH.

The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate isolated the prostate set of prostate cells of the subject that are differentially regulated compared to normal prostate tissue. (II) comprises from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the agent, preparing a second gene expression profiles cells, and comparing the first and second gene expression profiles. (II) is useful for diagnosing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH. The methods are useful to present information identifying the clevel of genes given in the specification in the tissue or cells to the topic of expression of gene in the database and displaying the conset.
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Best Local
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                      detecting expression levels of one or more genes in patient that are differentially regulated compared cells -
                                                                                                                                                                                                                                                                                                                                                                                 Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from
                                                                                                                                                                                                                                                                                                                   Disclosure; Page 207; 444pp; English.
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05-JUN-2001;
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2001US-0873319
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30-JUN-2000;
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19-MAY-2000;
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14-AUG-2000;
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14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence #144 encoding novel human connective tissue polypeptide
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14-AUG-2000;
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26-JUL-2000;
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17-MAR-2000;
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2000US-022577

2000US-022575

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2000US-0224518
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2000US-0217496
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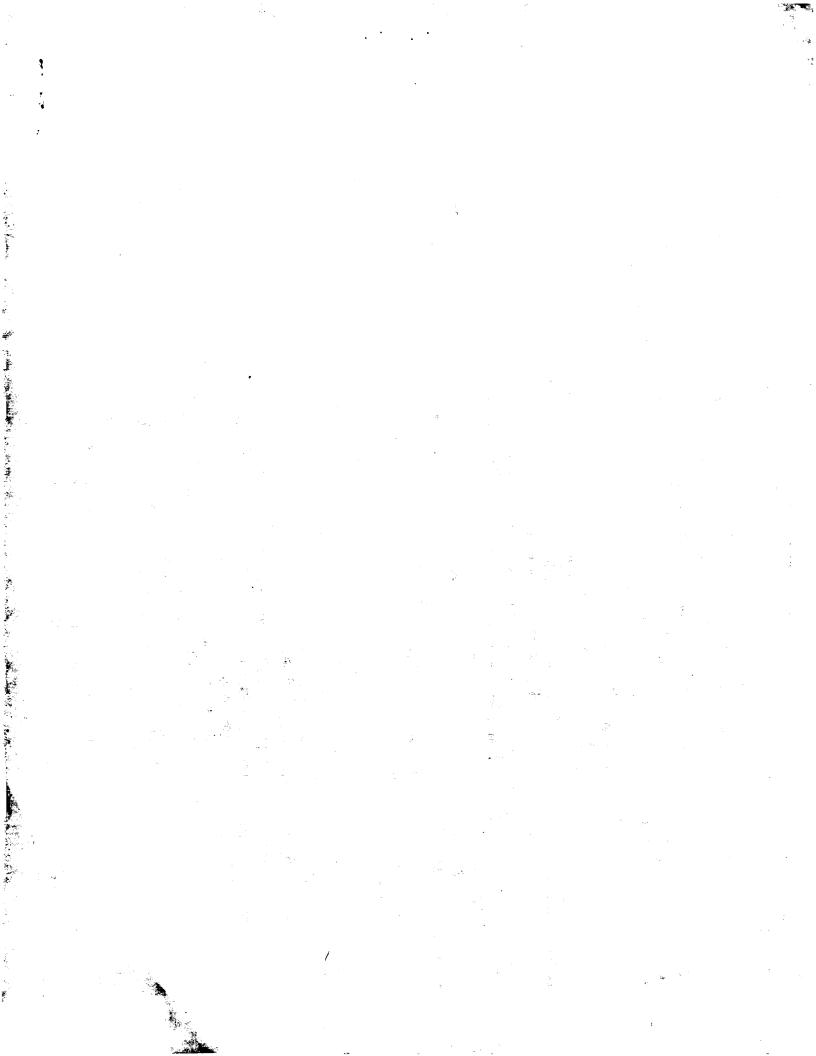
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used in
such as
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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
                                     The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                        CA,
                                                                                                                                                                                                                      acid encoding novel connective tissue associated diagnosing, preventing, treating or ameliorating cancer or rheumatoid arthritis -
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/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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12932
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6663
11832
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9 US-09-950-634-1

0 US-09-783-590-2469

9 US-10-040-739-549

10 US-09-864-761-12738

9 US-09-895-913A-245

9 US-09-764-872-812

9 US-09-764-872-813

10 US-09-815-242-8683

10 US-09-815-242-8681

10 US-09-815-242-8941
                                                                                                                                                     US-09-880-107-2006

US-09-764-847-1132

US-09-747-835A-12

US-09-037-657-28

US-09-037-657-38

US-09-969-708-561

US-09-880-107-3150

US-09-770-149-464
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2938.192 Million cell updates/sec
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                                                                                                                         Sequence 2006, Ap
Sequence 1132, App
Sequence 12, Appl
Sequence 28, Appl
Sequence 38, Appl
Sequence 3150, App
Sequence 464, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 2469, Ap
Sequence 245, App
Sequence 812, App
Sequence 813, App
Sequence 9123, Ap
Sequence 2683, Ap
Sequence 8867, Ap
Sequence 8941, Ap
                                                                                                                                                                                                                                                                                     Description
                                                                                                 Sequence 549, App
Sequence 12738, A
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## ALIGNMENTS

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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEO ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2006
TENGTH: 340
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                                                                                                                                             US-09-880-107-2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2006, Application US/09880107 Patent No. US20020142981A1
                                                                      Matches
                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Horne, Darci T. APPLICANT: Vockley, Josep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 H81070
NAME/KEY: unsure
LOCATION: (1)..(340)
OTHER INFORMATION: n = a or c or g or t
Local Similarity 87.5 es 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vockley, Joseph
Scherf, Uwe
                                                                                      61.9%;
87.5%;
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                                                                      0;
                                                                    Score 19.2; D
Pred. No. 13;
0; Mismatches
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                                                                                                       Length 340;
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RESULT 2 US-09-764-847-1132/c ; Sequence 1132, Application US/09764847

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                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (135)..(1601)
US-09-747-835A-12
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; ORGANISM: Homo sapiens
US-09-764-847-1132
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn
SEQ ID NO 12
LENGTH: 2936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1132
LENGTH: 12932
                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
EILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
ERIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/650,312
PRIOR APPLICATION NUMBER: US 09/650,312
PRIOR FILING DATE: 2000-00-08-31
PRIOR FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 09/552,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
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                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3205 GGGATTCTGACATGACAGTGCAATTGC 3179
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CGGAATTCTCACATGAGGGTGCATTTGC 29
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1 Similarity 81.5%;
22; Conservation
                                                                                    Similarity
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Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09747835A
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                        version 3.0
                                                                                                                                                                                                                                                                                                                                                               2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                        2000-04-25
                                                                                  59.4%;
78.6%;
                                                            Score 18.4; D
Pred. No. 44;
0; Mismatches
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US-09-037-657-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 6663
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application No. US20020045741A1
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Patent No.
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                                                                                               TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES TITLE OF INVENTION: ENCODING SAME FILE REFERENCE: DAVIES COLLISON CAVE (CIP) CURRENT APPLICATION NUMBER: US/09/037,657A CURRENT FILING DATE: 1998-03-10
                                                                                                                                                                                                                                                                                              APPLICANT: Alexander, Warren APPLICANT: Rakar, Steven APPLICANT: Rakar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES TITLE OF INVENTION: ENCODING SAME FILE REFERENCE: DAVIES COLLISON CAVE (CIP) CURRENT APPLICATION NUMBER: US/09/037,657A CURRENT FILING DATE: 1998-03-10
                                                          EARLIER APPLICATION NUMBER: 08/928,720 EARLIER FILING DATE: 1997-09-11
                                                                                                                                                                                                         APPLICANT: Maeda, Masatsugu
APPLICANT: Kikuchi, Yasufumi
APPLICANT: Nash, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hilton, Douglas
APPLICANT: Nicola, Nicos A.
  SOFTWARE: PatentIn Ver. 2.0 EQ ID NO 38
                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wilson,
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hilton, Douglas J. APPLICANT: Nicola, Nicos A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1997-09-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhang, Jian-Guo APPLICANT: Alexander, Warren
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Farley, Alison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nash,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Maeda, Masatsugu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Farley, Alison APPLICANT: Wilson, Tracy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2342 CGTCACTCTCACAGGAGGATCCATTTGC 2315
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nes 22; Conserv
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o. US20020045741A1
                                                                                                                                                                                                                                                                      Kojima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fabri, Louis
Kojima, Tetsuo
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Nash, Andrew
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Pred. No. 51
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US-09-969-708-561
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                                                                                                                                                                                                                                                                               US-09-880-107-3150
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                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                   Sequence 3150, Application US/09880107 Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 561
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                         CURRENT APPLICATION NUMBER: U5/09/880,11
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
                                                                                                                                     APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturing OF INVENTION: Sets
                           PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
                                                                                                                                                                                                                    APPLICANT: Horne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Sets FILE REFERENCE: 689290-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homosapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Unknown Organism: Murine NR6 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 11832
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                                                                                                                                                                                                                                                                                                                                                233
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 NO 3150
                                                                                                                                                                                                                                                                                                                                           TTCTCACATGAGGGTGCATTTGCCC
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              PatentIn Ver.
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80.0%;
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78.6%;
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Pred. No. 40;
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                                                                           RESULT 9
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SEQ ID NO 464
LENGTH: 661
             Sequence 1, Application US/09950634 Publication No. US20030032775A1 GENERAL INFORMATION:
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Best Local :
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APPLICANT: Molnar-Kimber, Katherine L.
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US-09-770-149-464/c; Sequence 464, Application US/09770149
                                                                                                                   ; ORGANISM: Arabidopsis thaliana US-09-770-149-464
                                                                                                                                                                                                                                                      APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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LOCATION: (1)..(470)
OTHER INFORMATION: n = a
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391 CTCACATGATGGTGCATCGGCCC
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                             9 CTCACATGAGGGTGCATTTGCCC
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20; Conserv
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Davis, Keith R.
Allen, Keith
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Haas, William David
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Hamilton, Carol
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                                                           Conservative
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87.0%;
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                                                                       Score 18.2;
Pred. No. 4
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Pred. No. 40;
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GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
                                                                                                                                                                                                                                                                                RESULT 10
US-09-783-590-2469/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                           APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
                   CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
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SEQUENCE CHARACTERISTICS:
LENGTH: 7653 base pairs
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3128 CAGAATTCTCTCATGAGGGTGACTAT 3103
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APPLICATION NUMBER: US 08/471,112
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-FEB-1995
APPLICATION NUMBER: US 08/312,023
APPLICATION NUMBER: US 08/312,023
APPLICATION NUMBER: US 08/207,975
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/950,634
FILING DATE: 13-Sep-2001
CLASSIFICATION: CUnknown>
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TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                        Haseltine, William A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Siekman, Michael T.
REGISTRATION NUMBER: 36,276
REFERENCE/DOCKET NUMBER: 01142.0058-00000
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Nakanishi, Koji
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Pred. No. 80;
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                                                                               and Expression Products 16.2
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US-10-040-739-549
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Best Local S
Matches 19
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PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2469
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (226)
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
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les 19; Conserv
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/040,739
EILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                             Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
NUMBER OF SEQUENCES: 1519
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jacobs, Kenneth
                                                                                      COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            COUNTRY: U.S.A
ZIP: 02140
                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                CITY: Cambridge
                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
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90.5%;
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Pred. No. 57;
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                                                                                                                                                                                                                                               Inc.
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TOPOLOGY: linear;

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 549:
US-10-040-739-549
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US-09-864-761-12738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                   PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 549:
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TELECOMPUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
DRMATION FOR SEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
                                                        FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                           APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00666
                                          FILING DATE:
                                                                                                                   APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Brown, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel, Luca
Hanzel, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                         2001-01-30
                                          2001-01-30
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75.9%;
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Pred. No. 57;
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; LOCATION: (54).
US-09-895-913A-245
RESULT 14
US-09-764-872-812
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Best Local Similarity /3...
"""" Conservative
                                                                                                                                                                                                                                                                                                      SEQ ID NO 245
LENGTH: 3666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 12738 LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 245, Application US/09895913A Patent No. US20020160456A1
                                                                                                                                 Matches
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OTHER INFORMATION: E
OTHER INFORMATION: E
OTHER INFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/895,913A CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of Polynucleotides TITLE OF INVENTION: Encoding No. US20020160456Alel HTITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/881,227 PRIOR FILING DATE: 1997-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 06132/043002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AL161747.1 OTHER INFORMATION: EXPRESSED IN PLAC OTHER INFORMATION: EXPRESSED IN FETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                       ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                364 GGCACGCTCATATCAGGGAGCATTTTCCC 336
                                                                                                                                                   Local
                                                                                3 GGAATTCTCACATGAGGGTGCATTTGCCC 31
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                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oomen, Raymond P.
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                                                                                                                                 Conservative
                                                                                                                                                                                                                  ...(3608)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.48;
75.98;
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75.98;
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Pred. No. 63;
0; Mismatches
                                                                                                                                                 Score 17.8; I
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AL = 0.83
AL = 0.82
AL = 0.99
                                                                                                                                                                   Length 3666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter Polypeptides in
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Sequence 812, Applica Publication No. US200 GENERAL INFORMATION: APPLICANT: Rosen et

Application US/09764872

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
FITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA125
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 957
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 813
LENCTH: 31718
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-872-813
                                                                                       В
                                                                                                                           δ
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; ORGANISM: Homo sapiens
US-09-764-872-812
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S-09-764-872-813

Sequence 813, Application US/09764872

Publication No. US20030050231A1

GENERAL INFORMATION:
earch completed: March 23, 2003, 17:17:01 ob time : 29.1818 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PA125
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 957
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 812
LENGTH: 31718
                                                                                                                                                              Query Match 57.4%; Score 17.8; DB 9; Length 31718; Best Local Similarity 75.9%; Pred. No. 1.3e+02; Matches 22; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 57.4%; Score 17.8; DB 9; Best Local Similarity 75.9%; Pred. No. 1.3e+02; Matches 22; Conservative 0; Mismatches 7;
                                                                            Length 31718;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                      Score
                        23
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21.2
  \begin{array}{c} 21 \\ 20.6 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      March 23, 2003, 14:20:51; Search time 201.545 Seconds (without alignments) 2491.051 Million cell updates/sec
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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gb_est2:*
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gb_est3:*
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12
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 AJ474604

10 AV835621

12 BE885242

17 AQ349812

17 AQ349812

12 BF796120

13 BG955224
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AJ474604 AJ474604
AV835621 AV835521
BE885242 601506309
AQ349812 RPCI11-11
BF796120 602258969
BG955224 CM4-CT065
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9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.	9.		9.	20	20	20	20	20	20	20	20		20.4	0
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AQ773452	AQ947577	A2216857	TA349G04Q	BI205055	BI205561	TA322C06Q	н81070	BB013755	BF572068	BQ202621	AZ866355	AZ238089	BE375801	BQ162047	BE101831	BM138265	BQ782041	AK014843	CNS0481D	AL602876	вQ187619	вQ638029	вм719600	вм682898	AQ420157	AQ198424	AV165009	BM044630	BQ720141	в0719125	CNS02FVQ	BI935904	AQ378111	BI921507	AZ521201	111	)51	AW128188
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## ALIGNMENTS

	FEATURES		JOURNAL COMMENT	AUTHORS	REFERENCE		SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	LOCUS
/organism="Hordeum vulgare" /db_xref="taxon:4513" /clone="\$0000800117607F1" /clone_lib="\$00008" /tlssue_type="Callus"	Location/Qualifiers 1420	Institute of Biotechnology University of Helsinki P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014, Finland	Unpublished (2002) Contact: Schulman AH	Saren, AM., Tanskanen, J., Paulin, L. and Schulman, A.H. Barley EST's	1 (bases 1 to 420)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae Trifficae: Hordanm	Hordeum vulgare. Hordeum vulgare	AJ474604.1 GI:21190560 EST.	sequence. AJ474604	AJ474604 420 bp mRNA linear EST 24-MAY-2002 AJ474604 S00008 Hordeum vulgare cDNA clone S0000800117G07F1, mRNA

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Mammalia; Eutheria;
                                                                                       mRNA sequence.
BE885242
                                                                                                          BE885242 1119 bp mRNA linear EST 20-OCT-: 601506309F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907851 5'
                                                                                                                                                                                                                                                          l Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
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AV835621
                           Homo sapiens
                                                                       BE885242.1 GI:10334018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kazsato@rib.okayama-u.ac.jp,
URL.http://www.rib.okayama-u.ac.jp/barley/
database:http://www.shigen.nig.ac.jp/barley/Barley.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barley EST sequencing project in NIG Unpublished (2001)
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/dev_stage="adult, heading stage"
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/clone="bah13i10"
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103 c ]
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                                                                                                                                                                                                                     Unpublished (1997)
Other_GSSs: RPCIII-118N20.TV
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
                                                 library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                 Class: BAC ends.
                                   Seq primer: SP6
                                                                                                                                               Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                      Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                         Map Building
                                                                                                                                                                                                                                                                                                                                                                                              Zhao, S., Adams, M.D.,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Location/Qualifiers
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a 291 c 305 g 42 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:3907851"
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/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
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                              3 GGAATTCTCACATGAGGGTGCATTTGCCC 31
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                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM9957 row: i column: 17
                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 13
High quality sequence stop: 628
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 984)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                               Conservative
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                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4342360"
/clone_1ib="NIH_MGC.85"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="Drgan: lymph; Vector: pcMv-SPORT6; Site_1: NotI;
/note="Organ: lymph; Vector: pcMv-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
48 a 263 c 290 g 183 t
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
166 c 137 g 246 t 2 others
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/clone="RPCI-11-118N20"
/clone_lib="RPCI-11"
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                                                            AW128188 52 fillf07.xl Sugano Kawakami 2600869 3' similar to conta
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                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases
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85.2%;
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220 GAAATCTCACATGAGGGTTTATTTCCC 246
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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120201-861-g10&t3=2001-02-12&t4=1)
Seq primer: puc 18 forward
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55 c 68 g 165 t
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/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
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/db_xref="taxon:9606"
/clone_lib="CT0657"
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E., Garcia Correa, R., Verjovski-Almeida, S.,
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      Marra, M.,
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 704)
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Contact: S.L. Johnson
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                                                                                                                         Mus musculus
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Library constructed by Dr. Sumio Sugr
Sequencing by: Washington University
Seq primer: T7 ET from Amersham
                                                                                                                                                                                                             AI226051.1 GI:3809104
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Fax: 314 286 1810
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                                                                                                                                                       house mouse
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//lab_host="MIDB (phage resist
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74 g 169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="mixed (one male and one unfertilized eggs)"
/dev_stage="adult"
   Hillier, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:7955"
/clone="2600869"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
/strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Danio.
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85.2%;
   Allen,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20.6;
Pred. No. 1.
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University Genome Sequencing Center
Bowles, M., Dietrich, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
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EST.

Populus balsamifera subsp. trichocarpa.

Populus balsamifera subsp. trichocarpa

Populus balsamifera subsp. trichocarpa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
                                                                  Hertzberg,M., Aspeborg,H., Erlandsson,R., Bjorkbacka,H., Hiltonen,T., Karlsson,J., Teeri,T., Gustafsson,P., Bahlerao,R., Jansson,S., Nilsson,O., Sundberg,B., Nilsson,P., Uhlen,M., Sandberg,G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI121740
BI121740.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI121740 206
F045P75Y Populus flower cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
    Location/Qualifiers
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This clone is available royalty free through LLNL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse
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21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality
                                                                                                                                                                                            (bases 1 to 206)
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   expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab.host="DHIOB"

//lab.host="Driogn": liver; Vector: pME18S-FL3; Site_1: DraIII

//note="Organ: liver; Vector: pME18S-FL3; Site care constant 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consortium (info@image.llnl.gov)
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/db_xref="taxon:10090"
/clone="IMAGE:1891339"
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/sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:18005715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
This BAC end was generated during the R&D process and may have
higher chance of clone tracking errors.
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Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
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Contact: Erlandsson
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The Institute for Genomic Research
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Fax: 46 8 245452
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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ss: BAC ends.
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                   a
/cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: ECORI;
/note="Data.ecorical content of the pBACe3.6; Site_1: ECORICAL content of the 
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/clone_lib="Populus flower cDNA library"
/note="Organ: flower"
29 c 53 g 47 t
                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="RPCI-11-461110"
/clone_lib="RPCI-11"
                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="GDB:7676841"
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EST541410
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BI921507
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A.,
J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Mari
,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato callus tissue (2001)
 RPCI-11-162C15.TJ RPCI-11 Homo
                  AQ378111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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Contact: CUGI
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                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="tomato callus"
/tissue_type="callus"
/dev_stage="25-40 days old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4081"
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                                                                                                                                                                                 Lycopersicon esculentum

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                           Unpublished (2001)
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                       Contact: CUGI
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Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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1 (bases 1 to 589)
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
RPCII1 Human Male BAC Library"
1 121 c 137 g 153 t 1 others
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                                                     This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fizam
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This clone is available through the Clemson University Genomics
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100 Jordan Hall, Clemson, SC 29634, USA
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XhoI; supplier: Cornell University; sequencing: '
/organism="Tetraodon nigroviridis'
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E 1 (bases 1 to 899)

E 1 (bases 1 to 899)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM13592 row: d column: 13

High quality sequence stop: 678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        899 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8232632 Lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6191580 5', mRNA sequence.
BQ719125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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                                                                                                                                                               230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                        5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="135M02"
/clone_lib="G"
/clone_lib="G"
/note="Genoscope sequence ID : COAG135BG01SP1-end :
PUC-Ori"
                                                                                                                                                           Technologies.
                                                                                                                                                                                                                                                                                              /note-"Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6191580"
                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lupski_sympathetic_trunk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:99883"
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                                                                             64.5%;
82.1%;
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                                                           Score 20; DB 14; 1
Pred. No. 3.6e+02;
0; Mismatches 5;
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Pred. No. 3.5e+02;
                                                                                                                                                           249 g
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                                                                                                                                                             244 t
                                                                                                DB 14; Length 899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                           Indels
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                                                           0;
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Db 346 GAATTCCCACAGGGAGGTGCATTTGTCC 373

Search completed: March 23, 2003, 17:12:25 Job time: 206.545 secs

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